

Two searched: attached
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09/14/92 135

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: JANE ZARRA Examiner #: 77512 Date: 12/13/02
Art Unit: 1635 Phone Number 30 6-5820 Serial Number: 09/910 185
Mail Box and Bldg/Room Location: 11 DC Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: AS Model of Chemical Oxygenizer - 3

Inventors (please provide full names): Bennett et al

Earliest Priority Filing Date: 7/18/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Seq ID No: 3
- unlimited size search
- limit to 100 NT

Therbo

Point of Contact:
Beverly Shears
Technical Info. Specialist
CMT 1E05 Tel: 308-4994

NA-5055

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	Type of Search	Vendors and cost where applicable
Searcher: <u>Beverly 24994</u>	NA Sequence (#) _____	STN _____
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Date Completed: <u>12-11-02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>5</u>	Fulltext _____	Sequence Systems _____
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Online Time: <u>20</u>	Other _____	Other (specify) <u>CGN</u>

PTO-1590 (8-01)

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 01:25:16 ; Search time 8359 Seconds

(without alignments)
17599.555 Million cell updates/sec

Title: US-09-910-185-3

Perfect score: 5055

Sequence: 1 cgatactacggggcatttt.....accctcttttaaaaaaa 5055

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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c 213	23.2	0.5	93	6	AX167441	Sequence	c 286	22.6	0.4	73	6	AX342432	AX342432 Sequence
c 214	23.2	0.5	97	6	AR068361	Sequence	c 287	22.6	0.4	75	6	I49876	I49876 Sequence 72
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c 217	23	0.5	68	6	AR007249	Sequence	c 290	22.6	0.4	79	6	AX057968	AX057968 Sequence
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c 226	23	0.5	82	6	AR075883	Sequence	c 299	22.6	0.4	93	9	AF172209	AF172209 Perodicti
c 227	23	0.5	82	6	AR097672	Sequence	c 300	22.6	0.4	93	9	HUMGSTF	M21866 Human gluta
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c 230	23	0.5	85	6	AR074468	Sequence	c 303	22.6	0.4	97	10	AF417933S1	G33091 Eb84975 Hum
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c 236	23	0.5	89	6	AR143516	Sequence	c 309	22.4	0.4	60	3	AF320168	AF320168 Drosophi
c 237	23	0.5	89	6	AR171420	Sequence	c 310	22.4	0.4	65	6	AX484855	AX484855 Sequence
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c 239	23	0.5	90	6	AX088777	Sequence	c 312	22.4	0.4	65	6	AX486057	AX486057 Sequence
c 240	23	0.5	91	6	HS033802	Human immat	c 313	22.4	0.4	67	4	S67757	S67757 prostaeycli
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c 246	23	0.5	96	10	Y033555S12	Mus muscu	c 319	22.4	0.4	81	6	AX022983	AX022983 Sequence
c 247	23	0.5	96	14	S51471S1	Sequence	c 320	22.4	0.4	89	6	AX046264	AX046264 Sequence
c 248	23	0.5	99	6	AX080697	Sequence	c 321	22.4	0.4	89	6	AX052945	AX052945 Sequence
c 249	23	0.5	99	6	I14151	Sequence 3	c 322	22.4	0.4	90	5	AF035412	AF035412 Xiphophor
c 250	23	0.5	99	6	I14152	Sequence 4	c 323	22.4	0.4	90	5	XX082796	U82796 Xiphophor
c 251	23	0.5	99	9	AY006143	Homo sapi	c 324	22.4	0.4	91	9	HSNJ10679	AT010679 Homo sapi
c 252	23	0.5	99	10	MM001105	Mus muscu	c 325	22.4	0.4	92	3	BME1BR3	AY00097 Flibroin gen
c 253	23	0.5	100	9	AJ8146	Human satel	c 326	22.4	0.4	93	10	RNU08886	U00886 Rattus norv
c 254	23	0.5	100	9	HSAT05	Sequence	c 327	22.4	0.4	94	1	STU06132	U06132 Salmonella
c 255	23	0.5	100	14	AB032317	Sequence	c 328	22.4	0.4	94	5	MTABAI8B	X95045 A.baeti mit
c 256	22.8	0.5	50	6	AR032644	Sequence	c 329	22.4	0.4	94	5	MTATRI8B	X95044 A.medirostr
c 257	22.8	0.5	50	6	AR032654	Sequence	c 330	22.4	0.4	94	5	MTATRI8B	X95044 A.transmont
c 258	22.8	0.5	50	6	AR209308	Sequence	c 331	22.4	0.4	94	5	MTATRI8B	X95046 A.rutemus
c 259	22.8	0.5	50	6	AR209318	Sequence	c 332	22.4	0.4	94	5	MTATRI8B	X95049 P.kautmanni
c 260	22.8	0.5	50	6	I29384	Sequence 25	c 333	22.4	0.4	94	5	MTATRI8B	X95050 P.spathula
c 261	22.8	0.5	50	6	I29394	Sequence 25	c 334	22.4	0.4	95	6	A36801	A36801 Sequence 20
c 262	22.8	0.5	50	6	I91058	Sequence 25	c 335	22.4	0.4	95	6	AR075879	AR075879 Sequence
c 263	22.8	0.5	57	10	I91068	Sequence 26	c 336	22.4	0.4	95	6	AR097668	AR097668 Sequence
c 264	22.8	0.5	57	10	RNU59456	Rattus norv	c 337	22.4	0.4	96	6	A08909	A08909 H.sapiens (
c 265	22.8	0.5	65	6	AX485349	Sequence	c 338	22.4	0.4	96	6	I73509	I73509 Sequence 12
c 266	22.8	0.5	71	5	LIRN28D8	Sequence	c 339	22.4	0.4	98	6	BD011910	BD011910 Ameliorat
c 267	22.8	0.5	75	5	XM082797	Sequence	c 340	22.4	0.4	98	6	BD011916	BD011916 Therapeut
c 268	22.8	0.5	75	5	XM082802	Sequence	c 341	22.4	0.4	98	6	BD012027	BD012027 Therapeut
c 269	22.8	0.5	76	6	AR003787	Sequence	c 342	22.4	0.4	98	6	BD012914	BD012914 Inhibiti
c 270	22.8	0.5	76	6	AR010123	Sequence	c 343	22.4	0.4	98	6	E23310	E23310 Antibody ag
c 271	22.8	0.5	76	6	AR055329	Sequence	c 344	22.4	0.4	98	6	E27079	E27079 Remedy for
c 272	22.8	0.5	76	6	AR055329	Sequence	c 345	22.4	0.4	98	23	BD004390	BD004390 Ameliorat
c 273	22.8	0.5	76	6	AR141258	Sequence	c 346	22.4	0.4	98	23	BD004446	BD004446 Therapeut
c 274	22.8	0.5	76	6	AR141495	Sequence	c 347	22.4	0.4	98	23	BD004507	BD004507 Therapeut
c 275	22.8	0.5	76	6	I11969	Sequence 81	c 348	22.4	0.4	98	23	BD008340	BD008340 Inhibiti
c 276	22.8	0.5	76	6	I40540	Sequence 79	c 349	22.4	0.4	99	6	AX023606	AX023606 Sequence
c 277	22.8	0.5	83	9	S59798S13	Sequence	c 350	22.4	0.4	99	6	AX160861	AX160861 Sequence
c 278	22.8	0.5	85	12	SYNSLMTIRE	Sequence	c 351	22.2	0.4	51	6	AX204250	AX204250 Sequence
c 279	22.8	0.5	86	6	AR042803	Sequence	c 352	22.2	0.4	56	6	AX381233	AX381233 Sequence
c 280	22.8	0.5	86	6	AX039266	Sequence	c 353	22.2	0.4	57	6	AR014088	AR014088 Sequence
c 281	22.8	0.5	99	6	AX080700	Sequence	c 354	22.2	0.4	57	6	AR117057	AR117057 Sequence
c 282	22.8	0.5	99	9	AB016201	Sequence 8	c 355	22.2	0.4	57	6	AR117058	AR117058 Sequence
c 283	22.8	0.5	99	10	RN078142	Sequence	c 356	22.2	0.4	57	6	I06477	I06477 Sequence 14
c 284	22.6	0.4	59	6	E13421	Sequence	c 357	22.2	0.4	57	6	I20517	I20517 Sequence 51

C 358	22.2	0.4	57	6	120518	Sequence 52	431	22	0.4	80	6	E29111	E29111 Kit for dia
C 359	22.2	0.4	58	6	AX358700	Sequence	C 432	22	0.4	81	6	I86928	I86928 Sequence 17
C 360	22.2	0.4	58	6	AX358701	Sequence	C 433	22	0.4	81	6	HUM5F08M3	D17624 Human Hep2
C 361	22.2	0.4	58	6	AX358707	Sequence	C 434	22	0.4	81	6	HSU5088	U505088 Human Hep2
C 362	22.2	0.4	58	6	AX358708	Sequence	C 435	22	0.4	82	5	AF044801	AF044801 Lampetra
C 363	22.2	0.4	58	6	AX358713	Sequence	C 436	22	0.4	84	6	A46818	A46818 Sequence 15
C 364	22.2	0.4	58	6	AX358714	Sequence	C 437	22	0.4	86	9	PH85592S08	PH85592S08
C 365	22.2	0.4	60	6	AX382509	Sequence	C 438	22	0.4	88	14	APH0V15E	APH0V15E
C 366	22.2	0.4	60	6	AX382518	Sequence	C 439	22	0.4	89	6	A39999	A39999 Foot and mo
C 367	22.2	0.4	64	6	AX0801	Sequence 11	C 440	22	0.4	89	6	A46511	A46511 Sequence 4
C 368	22.2	0.4	64	9	AP328551	Homo sapi	C 441	22	0.4	90	5	XH082794	XH082794
C 369	22.2	0.4	66	6	AX080586	Sequence	C 442	22	0.4	90	5	XH082798	XH082798
C 370	22.2	0.4	67	6	AR072415	Sequence	C 443	22	0.4	90	5	XM082801	XM082801 Xiphophorus
C 371	22.2	0.4	67	6	I06253	Sequence 11	C 444	22	0.4	90	5	XM082805	XM082805 Xiphophorus
C 372	22.2	0.4	67	6	I26526	Sequence 21	C 445	22	0.4	90	5	XM082806	XM082806 Xiphophorus
C 373	22.2	0.4	69	6	AF039636	Ceratitis	C 446	22	0.4	91	3	DDIACCTIN8A	M25115 Dictyostell
C 374	22.2	0.4	69	6	AX179510	Sequence	C 447	22	0.4	92	6	AR203063	AR203063 Sequence
C 375	22.2	0.4	71	5	ACRN28D8	Amia calva	C 448	22	0.4	92	6	HSAC134	U22227 Human aggre
C 376	22.2	0.4	72	6	I49879	Sequence 78	C 449	22	0.4	93	9	HSAC134	U22227 Human aggre
C 377	22.2	0.4	73	5	AAARN28D8	Anguilla an	C 450	22	0.4	93	9	HSAC134	U22227 Human aggre
C 378	22.2	0.4	74	9	HUMDXSTR	Human DNA t	C 451	22	0.4	93	9	HSAC134	U22227 Human aggre
C 379	22.2	0.4	78	6	AX328771	Sequence	C 452	22	0.4	93	9	HSAC134	U22227 Human aggre
C 380	22.2	0.4	78	10	AF096391	Mus muscu	C 453	22	0.4	93	9	HSAC134	U22227 Human aggre
C 381	22.2	0.4	81	14	AF166728	Hepatitis	C 454	22	0.4	93	9	HSAC134	U22227 Human aggre
C 382	22.2	0.4	81	14	AF166734	Hepatitis	C 455	22	0.4	96	6	AR152238	AR152238 Sequence
C 383	22.2	0.4	81	14	AF166737	Hepatitis	C 456	22	0.4	96	6	AR152238	AR152238 Sequence
C 384	22.2	0.4	81	14	AF166744	Hepatitis	C 457	22	0.4	99	3	DROG28V	DROG28V
C 385	22.2	0.4	84	6	A35498	Synthetic 1	C 458	22	0.4	100	9	AY006225	AY006225
C 386	22.2	0.4	90	6	AR148129	Sequence	C 459	22	0.4	100	9	AY006326	AY006326
C 387	22.2	0.4	90	6	AX237216	Sequence	C 460	22	0.4	100	9	AY006328	AY006328
C 388	22.2	0.4	90	6	E12933	Sequence	C 461	22	0.4	100	9	HS45B4F	HS45B4F
C 389	22.2	0.4	90	6	E12933	Sequence	C 462	22	0.4	100	9	HS45B4F	HS45B4F
C 390	22.2	0.4	91	6	AX366434	Solid tumor	C 463	22	0.4	100	10	RNO230479	RNO230479
C 391	22.2	0.4	92	3	DEPROBO	Sequence 10	C 464	22	0.4	100	10	HS4310741	HS4310741
C 392	22.2	0.4	92	6	I72525	Sequence 10	C 465	22	0.4	100	10	HS4310741	HS4310741
C 393	22.2	0.4	93	8	BMU35417	Beauveria a	C 466	22	0.4	100	10	HS4310741	HS4310741
C 394	22.2	0.4	93	8	EA285D1	E. album 285	C 467	22	0.4	100	10	HS4310741	HS4310741
C 395	22.2	0.4	93	9	AB044123	Homo sapi	C 468	22	0.4	100	10	HS4310741	HS4310741
C 396	22.2	0.4	94	5	OM306956	Odontoph	C 469	22	0.4	100	10	HS4310741	HS4310741
C 397	22.2	0.4	95	14	E11248278	Echovirus	C 470	22	0.4	100	10	HS4310741	HS4310741
C 398	22.2	0.4	96	5	AF459837	Gallus ga	C 471	22	0.4	100	10	HS4310741	HS4310741
C 399	22.2	0.4	96	5	AF459838	Gallus ga	C 472	22	0.4	100	10	HS4310741	HS4310741
C 400	22.2	0.4	96	5	AF395211	Homo sapi	C 473	22	0.4	100	10	HS4310741	HS4310741
C 401	22.2	0.4	98	6	AX287661	Sequence	C 474	22	0.4	100	10	HS4310741	HS4310741
C 402	22.2	0.4	99	6	A74519	Sequence 20	C 475	22	0.4	100	10	HS4310741	HS4310741
C 403	22.2	0.4	99	6	A77498	Sequence 20	C 476	22	0.4	100	10	HS4310741	HS4310741
C 404	22.2	0.4	99	10	AF007843	Mus muscu	C 477	22	0.4	100	10	HS4310741	HS4310741
C 405	22.2	0.4	100	6	AX020436	Sequence	C 478	22	0.4	100	10	HS4310741	HS4310741
C 406	22.2	0.4	49	6	AS0141	Sequence 6	C 479	22	0.4	100	10	HS4310741	HS4310741
C 407	22.2	0.4	51	6	AX162504	Sequence	C 480	22	0.4	100	10	HS4310741	HS4310741
C 408	22.2	0.4	51	6	AX162874	Sequence	C 481	22	0.4	100	10	HS4310741	HS4310741
C 409	22.2	0.4	51	6	AX204235	Sequence	C 482	22	0.4	100	10	HS4310741	HS4310741
C 410	22.2	0.4	54	6	E59415	Signal pept	C 483	22	0.4	100	10	HS4310741	HS4310741
C 411	22.2	0.4	55	6	I13710	Sequence 16	C 484	22	0.4	100	10	HS4310741	HS4310741
C 412	22.2	0.4	57	6	AX012288	Sequence	C 485	22	0.4	100	10	HS4310741	HS4310741
C 413	22.2	0.4	61	6	AX381803	Sequence	C 486	22	0.4	100	10	HS4310741	HS4310741
C 414	22.2	0.4	65	6	AX483346	Sequence	C 487	22	0.4	100	10	HS4310741	HS4310741
C 415	22.2	0.4	66	6	AR007246	Sequence	C 488	22	0.4	100	10	HS4310741	HS4310741
C 416	22.2	0.4	66	6	AR062450	Sequence	C 489	22	0.4	100	10	HS4310741	HS4310741
C 417	22.2	0.4	66	6	AR170032	Sequence	C 490	22	0.4	100	10	HS4310741	HS4310741
C 418	22.2	0.4	66	6	AR170459	Sequence	C 491	22	0.4	100	10	HS4310741	HS4310741
C 419	22.2	0.4	66	6	I27736	Sequence 23	C 492	22	0.4	100	10	HS4310741	HS4310741
C 420	22.2	0.4	67	6	AR072442	Sequence	C 493	22	0.4	100	10	HS4310741	HS4310741
C 421	22.2	0.4	67	6	I26553	Sequence 24	C 494	22	0.4	100	10	HS4310741	HS4310741
C 422	22.2	0.4	68	6	AR161850	Sequence	C 495	22	0.4	100	10	HS4310741	HS4310741
C 423	22.2	0.4	74	6	A11918	nucleotide	C 496	22	0.4	100	10	HS4310741	HS4310741
C 424	22.2	0.4	74	6	A11920	nucleotide	C 497	22	0.4	100	10	HS4310741	HS4310741
C 425	22.2	0.4	75	5	XM082797	Xiphophorus	C 498	22	0.4	100	10	HS4310741	HS4310741
C 426	22.2	0.4	75	5	XM082804	Xiphophorus	C 499	22	0.4	100	10	HS4310741	HS4310741
C 427	22.2	0.4	75	5	XM082804	Xiphophorus	C 500	22	0.4	100	10	HS4310741	HS4310741
C 428	22.2	0.4	78	6	A11917	nucleotide	C 501	22	0.4	100	10	HS4310741	HS4310741
C 429	22.2	0.4	78	6	A11919	nucleotide	C 502	22	0.4	100	10	HS4310741	HS4310741
C 430	22.2	0.4	80	6	AB7762	Sequence 56	C 503	22	0.4	100	10	HS4310741	HS4310741

504	21.8	0.4	100	11	G32918	G32918 A009W25 Hum	577	21.4	0.4	84	9	HUMENL1	M14059 Human liver
505	21.8	0.4	100	11	HS309128	AJ309128 Homo sapi	c 578	21.4	0.4	85	6	AR030723	AR030723 Sequence
506	21.6	0.4	43	3	AAAN2	X15295 Anopheles a	579	21.4	0.4	87	6	A36803	A36803 Sequence 22
507	21.6	0.4	47	6	AX195036	AX195036 Sequence	580	21.4	0.4	87	6	AR075881	AR075881 Sequence
508	21.6	0.4	52	6	AX456490	AX456490 Sequence	581	21.4	0.4	87	6	AR097670	AR097670 Sequence
509	21.6	0.4	54	6	I13484	I13484 Sequence 18	582	21.4	0.4	87	13	M23845	M23845 Figure 3. N
510	21.6	0.4	57	7	pp7CIN2	M12222 Bacterioph	583	21.4	0.4	88	9	S79269	S79269 Duffly [huma
511	21.6	0.4	59	6	AR172733	AR172733 Sequence	c 584	21.4	0.4	88	11	AF021107	AF021107 Homo sapi
512	21.6	0.4	59	6	AR178677	AR178677 Sequence	585	21.4	0.4	89	6	AX068163	AX068163 Sequence
513	21.6	0.4	59	6	AR181248	AR181248 Sequence	c 586	21.4	0.4	89	9	HSYAP0G11	AX030211 Homo sapi
514	21.6	0.4	59	6	AR199929	AR199929 Sequence	c 587	21.4	0.4	90	6	AX052903	AX052903 Sequence
515	21.6	0.4	64	6	A60793	A60793 Sequence 10	588	21.4	0.4	90	8	AF176407	AF176407 Quercus f
516	21.6	0.4	70	6	AR174789	AR174789 Sequence	c 589	21.4	0.4	90	8	HSCE1F	X58162 Human T lym
517	21.6	0.4	72	6	AX366537	AX366537 Sequence	590	21.4	0.4	91	8	AF176404	AF176404 Quercus f
518	21.6	0.4	72	10	MUSCIA17	K03035 Mouse alpha	c 591	21.4	0.4	92	6	AR014058	AR014058 Sequence
519	21.6	0.4	73	6	E33309	E33309 Dsba/Dsba/D	c 592	21.4	0.4	92	6	I22008	I22008 Sequence 94
520	21.6	0.4	74	10	AF265986	AF265986 Mus muscu	c 593	21.4	0.4	92	14	HTU12104	HTU12104 Human T-cel
521	21.6	0.4	76	6	AX174956	AX174956 Sequence	c 594	21.4	0.4	94	6	AR140871	AR140871 Sequence
522	21.6	0.4	77	6	AX057282	AX057282 Sequence	c 595	21.4	0.4	94	6	AR150821	AR150821 Sequence
523	21.6	0.4	77	6	HSU29117	U29117 Human lipom	c 596	21.4	0.4	94	6	AX023633	AX023633 Sequence
524	21.6	0.4	79	8	CBE345109	AJ345109 Carpinus	c 597	21.4	0.4	94	6	AX182150	AX182150 Sequence
525	21.6	0.4	79	12	SYNML3PLK	K00611 plasmid pap	c 598	21.4	0.4	94	6	BD003074	BD003074 Polynucle
526	21.6	0.4	81	6	AR119865	AR119865 Sequence	c 599	21.4	0.4	94	6	I65699	I65699 Sequence 59
527	21.6	0.4	83	6	AX029378	AX029378 Sequence	c 600	21.4	0.4	94	6	I67931	I67931 Sequence 59
528	21.6	0.4	85	3	AY075043	AY075043 Polsonia	c 601	21.4	0.4	94	6	I90152	I90152 Sequence 59
529	21.6	0.4	87	6	AX278072	AX278072 Sequence	c 602	21.4	0.4	96	8	HVU234896	HVU234896 Hordeum v
530	21.6	0.4	88	6	AX146316	AX146316 Sequence	c 603	21.4	0.4	96	8	AF395211	AF395211 Homo sapi
531	21.6	0.4	88	8	S77500	S77500 Oxi3-cytoch	c 604	21.4	0.4	96	9	AF395792	AF395792 Homo sapi
532	21.6	0.4	90	5	AF035412	AF035412 Xiphophor	c 605	21.4	0.4	96	10	RATPWC3A32	RATPWC3A32
533	21.6	0.4	90	6	AX435642	AX435642 Sequence	c 606	21.4	0.4	97	6	A36806	A36806 Sequence 25
534	21.6	0.4	90	6	HSU5163	U5163 Human Isola	c 607	21.4	0.4	97	6	AR075884	AR075884 Sequence
535	21.6	0.4	90	14	AF106090	AF106090 Hepatitis	c 608	21.4	0.4	97	6	AR097673	AR097673 Sequence
536	21.6	0.4	90	14	AF106093	AF106093 Hepatitis	c 609	21.4	0.4	98	8	S66605	S66605 fclone t33.
537	21.6	0.4	90	14	AF106101	AF106101 Hepatitis	c 610	21.4	0.4	99	9	HSITGAD05	HSITGAD05 Human beta
538	21.6	0.4	90	14	AF106103	AF106103 Hepatitis	c 611	21.4	0.4	100	3	AG2H117	AG2H117 A.gambiae s
539	21.6	0.4	93	4	FCMYOS03	AF001618 Fells cat	c 612	21.4	0.4	100	6	AR119732	AR119732 Sequence
540	21.6	0.4	93	6	A28234	A28234 DNA cassette	c 613	21.4	0.4	100	6	AR129862	AR129862 Sequence
541	21.6	0.4	93	6	A28235	D78235 Homo sapien	c 614	21.4	0.4	100	9	F185592S15	F185592S15 Homo sapi
542	21.6	0.4	93	6	D78279S16	A60866 Sequence 17	c 615	21.4	0.4	100	9	HUMTHIS03	HUMTHIS03 Homo sapien
543	21.6	0.4	94	6	A60866	X67456 A. israeli	c 616	21.4	0.4	100	10	AR010314	AR010314 Mus muscu
544	21.6	0.4	95	1	AI1684	AX11975 Sequence	c 617	21.2	0.4	30	6	E30088	E30088 Human Bmp-7
545	21.6	0.4	95	6	AX11975	AX138024 Sequence	c 618	21.2	0.4	51	6	AX157484	AX157484 Sequence
546	21.6	0.4	95	6	AX138024	G31304 sy8991-19	c 619	21.2	0.4	51	6	AX163065	AX163065 Sequence
547	21.6	0.4	96	11	G31304	AX339342 Sequence	c 620	21.2	0.4	51	6	AX163066	AX163066 Sequence
548	21.6	0.4	97	6	AX339342	X14775 Human DNA f	c 621	21.2	0.4	51	6	AX189852	AX189852 Sequence
549	21.6	0.4	97	9	HSUJMEMH	X12620 Human unpro	c 622	21.2	0.4	51	10	AF005572	AF005572 Mus muscu
550	21.6	0.4	98	9	HSTRGM42	AB032277 TT virus	c 623	21.2	0.4	54	6	A62703	A62703 Sequence 4
551	21.6	0.4	98	14	AB032277	AX023653 Sequence	c 624	21.2	0.4	55	9	S76369	S76369 PML-RARA fu
552	21.6	0.4	99	6	AX023653	G71249 721694031FM	c 625	21.2	0.4	60	6	AR201911	AR201911 Sequence
553	21.6	0.4	99	11	G71249	AX162876 Sequence	c 626	21.2	0.4	60	9	S66488	S66488 NEFH-neurof
554	21.4	0.4	49	6	AX162876	AX139459 Sequence	c 627	21.2	0.4	62	6	I06254	I06254 Sequence 12
555	21.4	0.4	55	6	AX139459	AF014635 Sequence	c 628	21.2	0.4	63	6	AX108115	AX108115 Sequence
556	21.4	0.4	56	6	AX139459	AF014635 Sequence	c 629	21.2	0.4	64	6	AR073784	AR073784 Sequence
557	21.4	0.4	62	6	AR014635	AR078706 Sequence	c 630	21.2	0.4	64	6	AR208280	AR208280 Sequence
558	21.4	0.4	62	6	AR078706	BD010427 Chimeric	c 631	21.2	0.4	65	6	AX484900	AX484900 Sequence
559	21.4	0.4	62	6	BD010427	I07082 Sequence 8	c 632	21.2	0.4	65	6	AX485140	AX485140 Sequence
560	21.4	0.4	62	6	I07082	I26767 Sequence 98	c 633	21.2	0.4	65	6	AX485901	AX485901 Sequence
561	21.4	0.4	62	6	I26767	I83775 Sequence 15	c 634	21.2	0.4	69	6	I15666	I15666 Sequence 3
562	21.4	0.4	62	6	I83775	AX485948 Sequence	c 635	21.2	0.4	69	6	I36671	I36671 Sequence 3
563	21.4	0.4	65	6	AX485948	AF027108 Ustilago	c 636	21.2	0.4	71	6	AX047839	AX047839 Sequence
564	21.4	0.4	66	8	AF027108	Z18748 Scyllorhinu	c 637	21.2	0.4	72	6	AX150205	AX150205 Sequence
565	21.4	0.4	73	5	SCRN28D8	AR135603 Sequence	c 638	21.2	0.4	72	8	MILKTRND	MILKTRND Yeast mitoc
566	21.4	0.4	75	6	AR135603	AR135603 Sequence	c 639	21.2	0.4	72	8	AR195065	AR195065 Sequence
567	21.4	0.4	75	6	I32935	I32935 Sequence 5	c 640	21.2	0.4	73	6	AR195065	AR195065 Sequence
568	21.4	0.4	75	6	I32935	I32936 Sequence 6	c 641	21.2	0.4	73	6	AR212274	AR212274 Sequence
569	21.4	0.4	76	3	PFU06449	U06449 Plasmodium	c 642	21.2	0.4	73	6	AX277693	AX277693 Sequence
570	21.4	0.4	76	3	HSU91165	U91165 Homo sapien	c 643	21.2	0.4	73	9	F310192S01	F310192 Homo sapi
571	21.4	0.4	78	6	AR062571	AR062571 Sequence	c 644	21.2	0.4	73	9	HS238523	HS238523 Homo sapi
572	21.4	0.4	79	6	AR125976	AR125976 Sequence	c 645	21.2	0.4	74	6	A35497	A35497 Synthetic 1
573	21.4	0.4	79	6	I47296	I47296 Sequence 22	c 646	21.2	0.4	75	4	AF330199	AF330199 Sus scrofa
574	21.4	0.4	80	9	AF205192	AF205192 Homo sapi	c 647	21.2	0.4	79	1	AX033166	AX033166 Sequence
575	21.4	0.4	81	9	AF020775	AF020775 Homo sapi	c 648	21.2	0.4	79	6	AF213170	AF213170 Metagris
576	21.4	0.4	82	9	HUM6PDS03	M26750 Human gluco	c 649	21.2	0.4	79	6	AX033158	AX033158 Sequence

c 650	21.2	0.4	81	14	AF463312	Hepatitis	723	21	0.4	78	6	AX127961	AX127961 Sequence
c 651	21.2	0.4	82	6	AR074463	Sequence	724	21	0.4	78	10	AF265826	AF265826 Mus muscu
c 652	21.2	0.4	82	6	AR081143	Sequence	725	21	0.4	79	6	AX099452	AX099452 Sequence
c 653	21.2	0.4	82	6	AR085340	Sequence	726	21	0.4	79	6	AX233523	AX233523 Sequence
c 654	21.2	0.4	82	6	AR088088	Sequence	727	21	0.4	79	6	AX381268	AX381268 Sequence
c 655	21.2	0.4	82	6	AR104247	Sequence	728	21	0.4	79	10	RNENDARX2	RNENDARX2 Sequence
c 656	21.2	0.4	82	6	AR143511	Sequence	729	21	0.4	80	6	I34337	I34337 R. norvegicu
c 657	21.2	0.4	82	6	AR171415	Sequence	730	21	0.4	80	6	AB010657	AB010657 Homo sapi
c 658	21.2	0.4	82	6	AR171586	Sequence	731	21	0.4	81	6	I19250	I19250 Sequence 22
c 659	21.2	0.4	82	6	AF46118852	Sequence	732	21	0.4	81	6	I19273	I19273 Sequence 45
c 660	21.2	0.4	84	9	HSCR2AA	Homo sapi	733	21	0.4	81	14	AB045015	AB045015 Hepatitis
c 661	21.2	0.4	86	8	AR042809	Sequence	734	21	0.4	81	14	AF390588	AF390588 Hepatitis
c 662	21.2	0.4	86	8	AY06555852	Sequence	735	21	0.4	83	8	SIARN03	SIARN03 Stellaria m
c 663	21.2	0.4	87	6	AR007041	Sequence	736	21	0.4	84	6	AR052315	AR052315 Sequence
c 664	21.2	0.4	87	6	AR111065	Sequence	737	21	0.4	84	9	AB010648	AB010648 Homo sapi
c 665	21.2	0.4	87	6	AR208319	Sequence	738	21	0.4	84	10	MUSIGACH	M32002 Mus muscitu
c 666	21.2	0.4	87	6	I74981	Sequence 18	739	21	0.4	86	3	DDIAC7C	M29111 D. discoideu
c 667	21.2	0.4	87	9	AF129751	Homo sapi	740	21	0.4	86	6	AR006930	AR006930 Sequence
c 668	21.2	0.4	87	9	S55093	Ig C gamma	741	21	0.4	86	6	AR110954	AR110954 Sequence
c 669	21.2	0.4	88	9	U00823	Human Delta-	742	21	0.4	86	6	AX114858	AX114858 Sequence
c 670	21.2	0.4	88	17	HSMC23E05	H. sapiens D	743	21	0.4	86	6	I74870	I74870 Sequence 69
c 671	21.2	0.4	90	6	AX404025	Sequence	744	21	0.4	87	6	A20577	A20577 ompa signal
c 672	21.2	0.4	90	6	AX429828	Sequence	745	21	0.4	87	6	AR052316	AR052316 Sequence
c 673	21.2	0.4	90	9	D86115	Homo sapien	746	21	0.4	88	6	AR166010	AR166010 Sequence
c 674	21.2	0.4	90	10	MMVAF8F32J	M. musculus	747	21	0.4	88	6	AR208981	AR208981 Sequence
c 675	21.2	0.4	92	9	AY006095	Homo sapi	748	21	0.4	90	6	AR152236	AR152236 Sequence
c 676	21.2	0.4	92	9	HSSCN1BS6	Homo sapien	749	21	0.4	90	6	AX000947	AX000947 Sequence
c 677	21.2	0.4	92	14	MCA4184P	Caulliflowe	750	21	0.4	90	6	AX031090	AX031090 Sequence
c 678	21.2	0.4	93	6	AR026962	Sequence	751	21	0.4	90	12	SYNVP7BG2	M15262 Synthetic V
c 679	21.2	0.4	96	6	E07898	DNA fragmen	752	21	0.4	90	14	HSILP6	M74728 Herpes simp
c 680	21.2	0.4	96	10	AF041916	Mus muscu	753	21	0.4	90	14	HSILP6	M74729 Herpes simp
c 681	21.2	0.4	98	6	AX287659	Sequence	754	21	0.4	90	14	HSILP6	M74730 Herpes simp
c 682	21.2	0.4	98	10	MUSFC5F08	Sequence	755	21	0.4	92	6	AR026110	AR026110 Sequence
c 683	21.2	0.4	99	3	DPE2N	Mus spretus	756	21	0.4	92	6	AX028716	AX028716 Sequence
c 684	21.2	0.4	100	3	AF274568	X99276 T. marmocita	757	21	0.4	92	6	I39918	I39918 Sequence 5
c 685	21.2	0.4	100	3	TMBDNF	AF274568 Parametru	758	21	0.4	93	6	A44964	A15975 Nucletotide
c 686	21.2	0.4	100	6	AX260734	AX620734 Sequence	759	21	0.4	93	6	AR021453	A15975 Nucletotide
c 687	21.2	0.4	100	9	AJ8157	AX208157 Homo sapi	760	21	0.4	93	6	A15975	A15975 Nucletotide
c 688	21.2	0.4	31	6	AX249384	AX249384 Sequence	761	21	0.4	93	6	A44964	A15975 Nucletotide
c 689	21.2	0.4	41	6	AR009929	AR009929 Sequence	762	21	0.4	93	6	A44964	A15975 Nucletotide
c 690	21.2	0.4	41	6	I76254	I76254 Sequence 82	763	21	0.4	93	6	AR021453	AR021453 Sequence
c 691	21.2	0.4	42	10	S77048	S77048 T-cell rece	764	21	0.4	93	6	AR043015	AR043015 Sequence
c 692	21.2	0.4	45	6	E59414	E59414 Signal pept	765	21	0.4	93	6	AR087439	AR087439 Sequence
c 693	21.2	0.4	49	6	A50140	A50140 Sequence 5	766	21	0.4	93	6	AR161303	AR161303 Sequence
c 694	21.2	0.4	50	6	AX048289	AX048289 Sequence	767	21	0.4	93	6	AR184332	AR184332 Sequence
c 695	21.2	0.4	51	6	AX204161	AX204161 Sequence	768	21	0.4	93	6	I44863	I44863 Sequence 3
c 696	21.2	0.4	54	6	AX097529	AX097529 Sequence	769	21	0.4	93	6	I63006	I63006 Sequence 13
c 697	21.2	0.4	56	6	A36725	A36725 Sequence 13	770	21	0.4	93	6	I64455	I64455 Sequence 13
c 698	21.2	0.4	57	6	AX103649	AX103649 Sequence	771	21	0.4	93	6	I88759	I88759 Sequence 13
c 699	21.2	0.4	57	6	AR021455	AR021455 Sequence	772	21	0.4	93	9	AF172199	AF172199 Alouatta
c 700	21.2	0.4	64	6	AR043017	AR043017 Sequence	773	21	0.4	93	9	AF172200	AF172200 Ateles pa
c 701	21.2	0.4	64	6	AR161305	AR161305 Sequence	774	21	0.4	93	9	AF172201	AF172201 Callithrix
c 702	21.2	0.4	64	6	I63008	I63008 Sequence 13	775	21	0.4	93	9	AF172202	AF172202 Callithrix
c 703	21.2	0.4	64	6	I88761	I88761 Sequence 13	776	21	0.4	93	9	AF172203	AF172203 Callithrix
c 704	21.2	0.4	64	10	AF034891	AF034891 Rattus no	777	21	0.4	93	9	HSRNP72S09	HSRNP72S09
c 705	21.2	0.4	66	6	AX288035	AX288035 Sequence	778	21	0.4	93	10	AF041945	AF041945 Mus muscu
c 706	21.2	0.4	66	6	AF189382	AF189382 Homo sapi	779	21	0.4	94	6	AR021464	AR021464 Sequence
c 707	21.2	0.4	66	14	SHU29127	SHU29127 Suid herpes	780	21	0.4	94	6	AR043026	AR043026 Sequence
c 708	21.2	0.4	69	5	PDRN28D8	PDRN28D8	781	21	0.4	94	6	AR142712	AR142712 Sequence
c 709	21.2	0.4	69	5	APU09225	APU09225 Alouatta pa	782	21	0.4	94	6	AR161314	AR161314 Sequence
c 710	21.2	0.4	70	6	AX040910	AX040910 Sequence	783	21	0.4	94	6	I12358	I12358 Sequence 14
c 711	21.2	0.4	72	6	AX023608	AX023608 Sequence	784	21	0.4	94	6	I28193	I28193 Sequence 14
c 712	21.2	0.4	72	6	I34357	I34357 Sequence 56	785	21	0.4	94	6	I33967	I33967 Sequence 14
c 713	21.2	0.4	73	6	AR091365	AR091365 Sequence	786	21	0.4	94	6	I63017	I63017 Sequence 14
c 714	21.2	0.4	73	8	PKU240505	PKU240505 Physconla	787	21	0.4	94	6	I88770	I88770 Sequence 14
c 715	21.2	0.4	74	6	AR119456	AR119456 Sequence	788	21	0.4	94	9	HDMG5TG	HDMG5TG
c 716	21.2	0.4	76	6	I34356	I34356 Sequence 55	789	21	0.4	96	10	AF010223	AF010223 Mus muscu
c 717	21.2	0.4	76	10	AF265807	AF265807 Mus muscu	790	21	0.4	97	6	AX261816	AX261816 Sequence
c 718	21.2	0.4	76	14	REO2511	REO2511 Reovirus se	791	21	0.4	98	14	AB032283	AB032283 TT virus
c 719	21.2	0.4	78	6	AR174671	AR174671 Sequence	792	21	0.4	99	5	GGCOL11	GGCOL11
c 720	21.2	0.4	78	6	AR174673	AR174673 Sequence	793	21	0.4	99	6	AR161298	AR161298 Sequence
c 721	21.2	0.4	78	6	AR184249	AR184249 Sequence	794	21	0.4	99	6	AX322857	AX322857 Sequence
c 722	21.2	0.4	78	6	AR184370	AR184370 Sequence	795	21	0.4	99	14	AF111884	AF111884 HIV-1 iso

796	20.8	0.4	51	6	AX162154	Sequence	869	20.8	0.4	98	6	AX287658	Sequence	AX287658	Sequence
797	20.8	0.4	51	6	AX164995	Sequence	870	20.8	0.4	98	6	AX287664	Sequence	AX287664	Sequence
C 798	20.8	0.4	51	6	AX190100	Sequence	871	20.8	0.4	98	6	AX287665	Sequence	AX287665	Sequence
800	20.8	0.4	54	6	AE8171	Sequence	C 872	20.8	0.4	98	6	E36069	Sequence	E36069	Higher-order
801	20.8	0.4	54	6	E07203	Sequence	C 873	20.8	0.4	98	6	I49625	Sequence	I49625	Sequence
802	20.8	0.4	54	6	E13400	Sequence	C 874	20.8	0.4	99	5	GGCOL15	Sequence	GGCOL15	Sequence
803	20.8	0.4	54	6	E125365	Sequence	C 875	20.8	0.4	99	5	GGCOL15	Sequence	GGCOL15	Sequence
804	20.8	0.4	56	6	AX139459	Sequence	C 876	20.8	0.4	99	5	AR078745	Sequence	AR078745	Sequence
805	20.8	0.4	56	6	AR117941	Sequence	C 877	20.8	0.4	100	6	AR261833	Sequence	AR261833	Sequence
806	20.8	0.4	61	9	AB032803	Sequence	C 878	20.8	0.4	100	6	AR109037	Sequence	AR109037	Sequence
807	20.8	0.4	65	6	AA5267	Sequence	C 879	20.8	0.4	100	6	AR166596	Sequence	AR166596	Sequence
808	20.8	0.4	67	6	AR072420	Sequence	C 880	20.8	0.4	100	6	AR178084	Sequence	AR178084	Sequence
C 809	20.8	0.4	67	6	126531	Sequence	C 881	20.8	0.4	100	6	AR178084	Sequence	AR178084	Sequence
C 810	20.8	0.4	68	6	AR012359	Sequence	C 882	20.6	0.4	21	6	AX095834	Sequence	AX095834	Sequence
C 811	20.8	0.4	69	6	AF218767	Sequence	C 883	20.6	0.4	21	6	AX095835	Sequence	AX095835	Sequence
C 812	20.8	0.4	70	9	HSAL1SN	Sequence	C 884	20.6	0.4	31	6	E11402	Sequence	E11402	Primer, 9/1
C 813	20.8	0.4	72	6	AS0898	Sequence	C 885	20.6	0.4	37	6	AX097685	Sequence	AX097685	Sequence
814	20.8	0.4	72	6	AR072426	Sequence	C 886	20.6	0.4	37	6	AX166887	Sequence	AX166887	Sequence
C 815	20.8	0.4	72	6	126537	Sequence	C 887	20.6	0.4	37	6	AX167014	Sequence	AX167014	Sequence
C 816	20.8	0.4	73	6	MO8915	Sequence	C 888	20.6	0.4	44	6	E11301	Sequence	E11301	Sequence
C 817	20.8	0.4	73	6	MO8915	Sequence	C 889	20.6	0.4	46	3	LE1KPGRB	Sequence	LE1KPGRB	Sequence
C 818	20.8	0.4	74	6	MO8915	Sequence	C 890	20.6	0.4	47	6	AX195039	Sequence	AX195039	Sequence
C 819	20.8	0.4	74	6	E03955	Sequence	C 891	20.6	0.4	51	6	AX156814	Sequence	AX156814	Sequence
C 820	20.8	0.4	75	6	AX112906	Sequence	C 892	20.6	0.4	51	6	AX157507	Sequence	AX157507	Sequence
C 821	20.8	0.4	75	6	AX112907	Sequence	C 893	20.6	0.4	51	6	AX155548	Sequence	AX155548	Sequence
C 822	20.8	0.4	76	6	AX474734	Sequence	C 894	20.6	0.4	51	6	AX190148	Sequence	AX190148	Sequence
C 823	20.8	0.4	76	6	AX381220	Sequence	C 895	20.6	0.4	51	6	AX203990	Sequence	AX203990	Sequence
C 824	20.8	0.4	76	6	AF040227	Sequence	C 896	20.6	0.4	51	6	AX204000	Sequence	AX204000	Sequence
C 825	20.8	0.4	78	5	AF035411	Sequence	C 897	20.6	0.4	51	6	184400	Sequence	184400	Sequence
826	20.8	0.4	79	6	AF16159	Sequence	C 898	20.6	0.4	54	10	AF224107	Sequence	AF224107	Sequence
827	20.8	0.4	80	1	HALTRC	Sequence	C 899	20.6	0.4	54	10	AF224118	Sequence	AF224118	Sequence
C 828	20.8	0.4	80	6	AX068162	Sequence	C 900	20.6	0.4	56	6	A38976	Sequence	A38976	Sequence
C 829	20.8	0.4	80	6	117605	Sequence	C 901	20.6	0.4	56	6	AR054372	Sequence	AR054372	Sequence
C 830	20.8	0.4	80	6	AF062767	Sequence	C 902	20.6	0.4	56	6	AX139457	Sequence	AX139457	Sequence
C 831	20.8	0.4	81	3	LIMSREP14	Sequence	C 903	20.6	0.4	56	6	HSYCRBCH	Sequence	HSYCRBCH	Sequence
C 832	20.8	0.4	81	10	AF265744	Sequence	C 904	20.6	0.4	57	6	AX467167	Sequence	AX467167	Sequence
C 833	20.8	0.4	81	14	AF221237	Sequence	C 905	20.6	0.4	59	6	AR146500	Sequence	AR146500	Sequence
C 834	20.8	0.4	82	6	117606	Sequence	C 906	20.6	0.4	59	6	S78804	Sequence	S78804	Sequence
C 835	20.8	0.4	83	6	A64750	Sequence	C 907	20.6	0.4	60	6	AX404653	Sequence	AX404653	Sequence
C 836	20.8	0.4	83	6	AR161647	Sequence	C 908	20.6	0.4	60	9	AF011625	Sequence	AF011625	Sequence
C 837	20.8	0.4	83	11	G36392	Sequence	C 909	20.6	0.4	61	6	AR118194	Sequence	AR118194	Sequence
C 838	20.8	0.4	84	3	LIMSREP1	Sequence	C 910	20.6	0.4	62	5	E26097	Sequence	E26097	Novel DNA f
C 839	20.8	0.4	84	9	HUMDAH08M3	Sequence	C 911	20.6	0.4	62	5	I05585	Sequence	I05585	Sequence
840	20.8	0.4	84	9	HSU5108	Sequence	C 912	20.6	0.4	64	3	DMW3AS	Sequence	DMW3AS	Sequence
841	20.8	0.4	87	17	HSU5108	Sequence	C 913	20.6	0.4	64	6	AX080203	Sequence	AX080203	Sequence
842	20.8	0.4	89	6	AX381436	Sequence	C 914	20.6	0.4	65	4	AF137375	Sequence	AF137375	Sequence
843	20.8	0.4	91	10	AB010320	Sequence	C 915	20.6	0.4	65	4	AX482957	Sequence	AX482957	Sequence
C 844	20.8	0.4	92	6	A44963	Sequence	C 916	20.6	0.4	65	6	AX484851	Sequence	AX484851	Sequence
C 845	20.8	0.4	92	6	AX093633	Sequence	C 917	20.6	0.4	65	6	AR027783	Sequence	AR027783	Sequence
C 846	20.8	0.4	92	6	164454	Sequence	C 918	20.6	0.4	65	8	AR027783	Sequence	AR027783	Sequence
C 847	20.8	0.4	93	6	AR074458	Sequence	C 919	20.6	0.4	66	6	AR146499	Sequence	AR146499	Sequence
C 848	20.8	0.4	93	6	AR081138	Sequence	C 920	20.6	0.4	66	10	AF265963	Sequence	AF265963	Sequence
C 849	20.8	0.4	93	6	AR085335	Sequence	C 921	20.6	0.4	66	10	MMU84673	Sequence	MMU84673	Sequence
C 850	20.8	0.4	93	6	AR088083	Sequence	C 922	20.6	0.4	69	6	AL17956	Sequence	AL17956	Sequence
C 851	20.8	0.4	93	6	AR104242	Sequence	C 923	20.6	0.4	69	6	AX119978	Sequence	AX119978	Sequence
C 852	20.8	0.4	93	6	AR143506	Sequence	C 924	20.6	0.4	69	6	AX138027	Sequence	AX138027	Sequence
C 853	20.8	0.4	93	6	AR171410	Sequence	C 925	20.6	0.4	69	12	AF411478	Sequence	AF411478	Sequence
C 854	20.8	0.4	93	6	AR171581	Sequence	C 926	20.6	0.4	70	5	LPN28D8X	Sequence	LPN28D8X	Sequence
C 855	20.8	0.4	93	9	HSC1INR2	Sequence	C 927	20.6	0.4	70	6	AR123757	Sequence	AR123757	Sequence
C 856	20.8	0.4	93	10	RATWCR1B	Sequence	C 928	20.6	0.4	71	6	AA2300	Sequence	AA2300	Sequence
C 857	20.8	0.4	94	5	MTACAL18B	Sequence	C 929	20.6	0.4	71	6	AA2301	Sequence	AA2301	Sequence
C 858	20.8	0.4	94	5	MTACAL18B	Sequence	C 930	20.6	0.4	72	6	AB2289	Sequence	AB2289	Sequence
C 859	20.8	0.4	94	5	MTSAL18B	Sequence	C 931	20.6	0.4	72	6	AR063726	Sequence	AR063726	Sequence
C 860	20.8	0.4	94	5	MTPEL18B	Sequence	C 932	20.6	0.4	72	6	AR122149	Sequence	AR122149	Sequence
C 861	20.8	0.4	94	5	AX187852	Sequence	C 933	20.6	0.4	72	6	AR142607	Sequence	AR142607	Sequence
C 862	20.8	0.4	94	6	AX187852	Sequence	C 934	20.6	0.4	72	6	AX150235	Sequence	AX150235	Sequence
C 863	20.8	0.4	94	11	HSPE75H11	Sequence	C 935	20.6	0.4	72	6	AX474798	Sequence	AX474798	Sequence
C 864	20.8	0.4	95	1	CUEI33575	Sequence	C 936	20.6	0.4	72	6	130089	Sequence	130089	Sequence
C 865	20.8	0.4	95	6	AR033948	Sequence	C 937	20.6	0.4	72	9	AF189555	Sequence	AF189555	Sequence
C 866	20.8	0.4	95	6	AR175081	Sequence	C 938	20.6	0.4	73	9	AF132018	Sequence	AF132018	Sequence
C 867	20.8	0.4	97	6	AX032525	Sequence	C 939	20.6	0.4	73	9	AF132490	Sequence	AF132490	Sequence
C 868	20.8	0.4	98	6	HUMCG7B1	Sequence	C 940	20.6	0.4	73	9	AF132491	Sequence	AF132491	Sequence
					AR087170	Sequence	C 941	20.6	0.4	73	9	HSB07HLAI	Sequence	HSB07HLAI	Sequence

Db	7	CACCCGGGCACTTGGCTTCACACTTGCGCAGATCACAGGCCACGAGCCCCCTTCGCTGCCTCCC	66
QY	3091	TCCGAGGGCTTGCGCCCTGCTGTGTGCCGCGC	3123
Db	67	GTCGCCGACCTGECACAGCCGGGCGCTGCGGCGCC	99
RESULT 10			
LOCUS	173148		99 bp DNA
DEFINITION	Sequence 10 from patent US 5686239.		linear PAT 03-APR-1998
ACCESSION	173148		
VERSION	173148.1 GI:3009287		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 99)		
TITLE	Reyes,G.R., Tam,A.W. and Yarbough,P.O.		
JOURNAL	Hepatitis E virus peptides and methods		
FEATURES	Patent: US 5686239-A 10 11-NOV-1997;		
source	Location/Qualifiers		
	1..99		
BASE COUNT	12 a 46 c 29 g	12 t	
ORIGIN			
Query Match	0.5%, Score 27.4; DB 6;	Length 99;	
Best Local Similarity	55.9%; Pred. No. 7.8e+05;		
Matches	52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;		
QY	3031 CAGCCGACGATGCGCTGTGGCCACGCGCTGAAGAGGCCACGACCCTGCGGACAGGC	3090	
Db	7 CAGCCGCGCCACTTGCTGCTCCACTTGCGAGATCAGAGCCACAGGCCCTTCGCTGCTCCC	66	
QY	3091 TCCGAGGGCTGGCGCTGCTGCTGTGTGCCGCGC	3123	
Db	67 GTCCGCGACCTGCCACACGCGGGGCTGTGCGGCGC	99	
RESULT 11			
LOCUS	PTU18443/c		
DEFINITION	Pan troglodytes pre-Alu-integration site clone Chimpa62.	98 bp DNA linear PRI 13-NOV-1995	
ACCESSION	U18443		
VERSION	U18443.1 GI:841185		
KEYWORDS			
SOURCE	.		
ORGANISM	Pan troglodytes.		
REFERENCE	Pan troglodytes.		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.		
JOURNAL	1 (bases 1 to 98)		
REFERENCE	Arcolet,S.S., Deininger,P.L. and Batzer,M.A.		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 98)		
JOURNAL	Batzer,M.A., Kilroy,G.E., Richard,P.E., Shaikh,T.H., Desselte,T.D.,		
REFERENCE	Hoppens,C.L. and Deininger,P.L.		
AUTHORS	Structure and variability of recently inserted Alu family members		
TITLE	Nucleic Acids Res. 18 (23), 6793-6798 (1990)		
JOURNAL	Medline		
REFERENCE	91088248		
AUTHORS	2175877		
TITLE	3 (bases 1 to 98)		
JOURNAL	Arcolet,S.S., Wang,Z., Weber,J.L., Deininger,P.L. and Batzer,M.A.		
REFERENCE	Alu repeats: a source for the genesis of primate microsatellites		
AUTHORS	Genomics 29 (1), 136-144 (1995)		
TITLE	Journal		
REFERENCE	66079101		
AUTHORS	8530063		
TITLE	4 (bases 1 to 98)		
JOURNAL	Batzer,M.A., Rubin,C.M., Hellmann-Bumberg,U., Alegria-Hartman,M.,		
REFERENCE	Loefflang,E.P., Stern,J.D., Bazan,H.A., Shaikh,T.H., Deininger,P.L.		
AUTHORS	and Schmid,C.W.		
TITLE	Dispersion and insertion polymorphism in two small subfamilies of		

Best Local Similarity 66.1%; Pred. No. 9.2e+05;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 3473 GCCAGAGTTCATGCGCTCGAGAGCCTGCCCCGAGGCGAGCAAAACCGACTGCCC 3531
DB 29 GGCAGAGTTCATGCGCTCGAGAGTAAAGCGGAGGAGGAGCAAGTGGAGTGGCCC 87

RESULT 15

AX031011/c AX031011 99 bp DNA linear PAT 20-SEP-2000
LOCUS Sequence 13 from Patent W09806830.

DEFINITION AX031011
ACCESSION AX031011
VERSION AX031011.1 GI:10278406

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 99)
Weiss, A.S.
unclassified.

Patent: WO 9806830-A 13-19-FEB-1998;
UNIV SYDNEY (AU); WEISS ANTHONY STEVEN (AU)

Location/Qualifiers

FEATURES

1..99
/organism="unclassified"
/db_xref="taxon:32644"

BASE COUNT 20 a 38 c 22 g 19 t
ORIGIN

Query Match

Best Local Similarity 66.1%; Pred. No. 9.2e+05;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 3473 GCCAGAGTTCATGCGCTCGAGAGCCTGCCCCGAGGCGAGCAAAACCGACTGCCC 3531
DB 75 GGCAGAGTTCATGCGCTCGAGAGTAAAGCGGAGGAGGAGCAAGTGGAGTGGCCC 17

RESULT 16

AX031041/c AX031041 99 bp DNA linear UNA 20-SEP-2000
LOCUS Sequence 13 from Patent W09806830.

DEFINITION AX031041
ACCESSION AX031041
VERSION AX031041.1 GI:10278434

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 99)
Weiss, A.S.
unclassified.

Patent: WO 9806830-A 13-19-FEB-1998;
UNIV SYDNEY (AU); WEISS ANTHONY STEVEN (AU)

Location/Qualifiers

FEATURES

1..99
/organism="unclassified"
/db_xref="taxon:32644"

BASE COUNT 20 a 38 c 22 g 19 t
ORIGIN

Query Match

Best Local Similarity 66.1%; Pred. No. 9.2e+05;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 3473 GCCAGAGTTCATGCGCTCGAGAGCCTGCCCCGAGGCGAGCAAAACCGACTGCCC 3531
DB 75 GGCAGAGTTCATGCGCTCGAGAGTAAAGCGGAGGAGGAGCAAGTGGAGTGGCCC 17

RESULT 17

HSPE06C12 HSPE06C12 82 bp DNA linear STS 21-MAY-1998

DEFINITION H.sapiens flow-sorted chromosome 1 HindIII fragment, SC1PE06C12, sequence tagged site.

ACCESSION AL009338
VERSION AL009338.1 GI:2664501

KEYWORDS STS; single read.
SOURCE Homo sapiens.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 82)
Gregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E.

Direct Submission
Submitted (03-DEC-1997) E-mail contact: humquery@sanger.ac.uk

Vector: pBSISK+
Marker: sG828963 (Primer A: CAGCCGAGCTGCTCATCTC;
Primer B: GCTTGCCACACTCATATAC; amplicon size: 82 bp) was mapped

to chromosome 1 using Radiation Hybrid
panel Genebridge 4 (GB4).

Location/Qualifiers

1..82
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 25 a 20 c 20 g 17 t
ORIGIN

Query Match

Best Local Similarity 71.4%; Pred. No. 1.1e+06;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1742 TGAACACACTTGATCTCAGACTGAGAGAAACCATACGCTGTGA 1790
DB 18 TCATCAGACACACAGAAATTCACACTGAGAGAGCCTTATGAGCTTAA 66

RESULT 18

SSGRTPL SSGRTPL 88 bp DNA linear MAM 16-DEC-1994
LOCUS SSGRTPL

DEFINITION S. scrofa DNA for gamma-glutamyl transpeptidase (5' end).

ACCESSION X16533
VERSION X16533.1 GI:1954

KEYWORDS gamma-glutamyl transpeptidase.
SOURCE Sus scrofa.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 88)
Papandriopoulou, A., Frey, A. and Gassen, H.G.

Cloning and expression of gamma-glutamyl transpeptidase from
isolated porcine brain capillaries

Eur. J. Biochem. 183 (3), 693-698 (1989)

Medline 89377838
PUBMED 2476308

COMMENT See X55020 for continued cds (mRNA sequence).

FEATURES
source
1..88
/organism="Sus scrofa"

/db_xref="taxon:9823"
36..>88
/codon_start=1

/product="gamma-glutamyltranspeptidase"
/protein_id="CAA34536.1"

/db_xref="GI:602909"
/db_xref="SWISS-PROT:P20735"
/translation="MKKRYLLALAAVAALVLL"

BASE COUNT 13 a 32 c 24 g 19 t
ORIGIN

Copied from PCI US2003092 on 04-03-2004

KEYWORDS	repetitive DNA.
SOURCE	Hyla chrysoscelis.
ORGANISM	Hyla chrysoscelis. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Hylinae; Hyla.
REFERENCE	1 (bases 1 to 82) Krenz,J.D., Semlitsch,R.D., Gerhardt,H.C. and Mahoney,P.A.
AUTHORS	Isolation and characterization of simple sequence repeat loci in the gray tree frog, Hyla chrysoscelis
TITLE	Unpublished
JOURNAL	2 (bases 1 to 82) Krenz,J.D.
REFERENCE	Direct Submission
AUTHORS	Submitted (08-JUN-1999) Krenz J.D., Biological Sciences, Minnesota State University, Department of Biological Sciences, Minnesota State University, Mankato MN 56001, USA
JOURNAL	Location/Qualifiers
FEATURES	1..82 /organism="Hyla chrysoscelis" /isolate="11D2" /db_xref="taxon:30342" /country="USA:Missouri"
source	12..65 /rpt_family="simple sequence repeat, dinucleotide" /rpt_type=DIRECT /rpt_unit=12..13
repeat_region	28 a 23 c 28 g 3 t
BASE COUNT	28 a 23 c 28 g 3 t
ORIGIN	
Query Match	0.5%; Score 25.6; DB 5; Length 82;
Best Local Similarity	57.5%; Pred. No. 1.7e+06;
Matches	46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 2588	ACAGAAGGAGCAGCGCCGACACACATTCAGTCCGGCTACTTCAGACGCCGCTCCT 2647
Db	1 AGAAGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 60
QY 2648	CAGGATCTCGCCCTGCCTTC 2667
Db	61 GCAGCATCAGGCTCAGCATC 80
RESULT 30	
LOCUS	AR021158 84 bp DNA linear PAT 05-DEC-1998
DEFINITION	Sequence 7 from patent US 5789389.
ACCESSION	AR021158
VERSION	AR021158.1 GI:3975773
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 84) Tarasiewicz,D.G., Scholtz,B., Holzmayer,T.A. and Roninson,I.B.
AUTHORS	BC12 derived genetic elements associated with sensitivity to chemotherapeutic drugs
TITLE	Patent: US 5789389-A 7 04-AUG-1998;
JOURNAL	Location/Qualifiers
FEATURES	1..84 /organism="unknown"
BASE COUNT	11 a 38 c 23 g 12 t
ORIGIN	
Query Match	0.5%; Score 25.6; DB 6; Length 84;
Best Local Similarity	59.7%; Pred. No. 1.7e+06;
Matches	43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 2622	GGCTTACCTGAGCAGACCCGCTCTCTCAGGGATTCGCGCTTCTCCAGCGCGCTC 2681
Db	3 GGTCAACCTGAGACCCCTCGCCAGCGGGAGAGACTTCTCCGCGCTTACCGCGGACTT 62
QY 2682	CAGCGAGCGCTC 2693

[illegible]

TITLE	Internal de novo initiation sites of the hcv ns5b polymerase and use thereof
JOURNAL	Patent: WO 0183736-A 23 08-NOV-2001;
FEATURES	BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
source	Location/Qualifiers 1..93
BASE COUNT	/organism="Hepatitis C virus" /db_xref="taxon:11103" 2 a 7 c 82 t
ORIGIN	
Query Match	0.5%; Score 25.2; DB 6; Length 93;
Best Local Similarity	55.8%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches	48; Conservative 0; Mismatches 38;
OY	4861 TTTGTTTGGCGTGTGTTTGTGATGATTTAGCATCTCATCTCAGTACTG 4920
Db	8 TTTTGTGTTGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 67
OY	4921 AGATGTGTTTCATTTATATTCCTTTT 4946
Db	68 TTTCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 93
RESULT 35	
LOCUS	AX008878 94 bp DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 3 from Patent WO964585.
ACCESSION	AX008878.
VERSION	AX008878.1 GI:9996300
KEYWORDS	human.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 94)
JOURNAL	Kleim,J.P., Sibenhorn,G., Beltsch,H. and Riess,G. Novel angiotensin receptor, production and use thereof Patent: WO 9964585-A 3 16-DEC-1999; KLEIM JOERG PETER (DE); SIBENHORN GERTRUD (DE); HEITSCH HOLGER (DE); RIESS GUENTHER (DE); HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES	Location/Qualifiers 1..94
source	/organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	30 a 24 c 14 g 26 t
ORIGIN	
Query Match	0.5%; Score 25.2; DB 6; Length 94;
Best Local Similarity	57.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches	45; Conservative 0; Mismatches 33;
OY	138 TGTGAGCGAAGAAGCCGTTGCTCCAGCAGCCACTTCTAATGAGATGAAAGTCCTGGACA 197
Db	17 TATTGACAAAATGAAGTAGAGCATATTATCCACTCTCTAATTTTGATGAAGAACTCCAGTGC 76
OY	198 GACTATTCACAGAGAGAG 215
Db	77 TACTACAAACGAGCGAG 94
RESULT 36	
LOCUS	AL841018 96 bp DNA linear STS 17-JUL-2002
DEFINITION	Arabidopsis thaliana transposon insertion STS SW_3.28438, sequence tagged site.
ACCESSION	AL841018
VERSION	AL841018.1 GI:21911912
KEYWORDS	STS; STS, sequence tagged site.
SOURCE	Arabidopsis thaliana
ORGANISM	Arabidopsis thaliana
FEATURES	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

BASE COUNT		5	a	51	c	32	g	12	t
ORIGIN									
Query Match									
Best Local Similarity 0.5%; Score 25.2; DB 11; Length 100;									
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;									
Oy	2934	CGGGATGCCCCGAGCCGCGGGCGCCCTGCTCCAGTTCATNTGCCGAGAGAGTGCAG	2993						
Db	100	CGGGGTTCATCTTTCGCCGGAGAGACCGGACACCGGGCGGGGCGGAGGCCG	41						
Oy	2994	CGACGGGGAGCCACGAGCTACGGCGGGCCAC	3027						
Db	40	GGAACGGGGACCCGGCGGGCCACACCGCCG	7						
RESULT 38									
LOCUS	25	bp	DNA	linear	PRI	26-JUL-2000			
DEFINITION	Homo sapiens DNA-binding protein (GLI3) sense primer.								
ACCESSION	AJ270365.1 GI:9557940								
VERSION	human.								
KEYWORDS	human.								
SOURCE	Homo sapiens								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE	1 (bases 1 to 25)								
AUTHORS	Palm,K., Salin-Nordstrom,T., Levesque,M.F. and Neuman,T.								
TITLE	Fetal and adult human CNS stem cells have similar molecular characteristics and developmental potential								
JOURNAL	Brain Res. Mol. Brain Res. 78 (1-2), 192-195 (2000)								
MEDLINE	20351569								
PUBMED	10891600								
REFERENCE	2 (bases 1 to 25)								
AUTHORS	Palm,K.								
TITLE	Direct Submission								
JOURNAL	Submitted (04-OCT-1999) Surgery, Cedars Sinai Medical Center, 8700 Beverly Blvd., Los Angeles, CA 90048, US								
COMMENT	Related entry: M57609.								
FEATURES	location/Qualifiers								
source	1..25								
	/organism="Homo sapiens"								
	/db_xref="taxon:9606"								
misc-feature	1..25								
	/note="PCR sense primer for DNA-binding protein (GLI3)"								
BASE COUNT	5	a	8	c	6	g	6	t	
ORIGIN									
Query Match									
Best Local Similarity 0.5%; Score 25; DB 9; Length 25;									
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Oy	1031	GCAGCTTTCAGCAGTGGCTCCTA	1055						
Db	1	GCAGCTTTCAGCAGTGGCTCCTA	25						
RESULT 39									
LOCUS	98	bp	DNA	linear	PAT	18-NOV-2000			
DEFINITION	Sequence 9 from Patent WO0063373.								
ACCESSION	AX039308								
VERSION	AX039308.1 GI:11229413								
KEYWORDS	synthetic construct.								
SOURCE	synthetic construct								
ORGANISM	artificial sequences.								

REFERENCE 1 (bases 1 to 98)
 AUTHORS Finney,H.M. and Lawson,A.D.
 TITLE A method of altering the properties of a membrane-associated prote
 in by substitution of the transmembrane domain
 JOURNAL Patent: WO 0063373-A 9 26-OCT-2000;
 CELLTECH THERAPEUTICS LIMITED (GB)
 FEATURES
 source 1..98
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="B6463"

BASE COUNT 2 a 37 c 25 g 34 t
 ORIGIN

Query Match 0.5%; Score 25; DB 6; Length 98;
 Best Local Similarity 58.9%; Pred. No. 2.2e+06;
 Matches 43; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2568 CACTATGCTGAACATGCTCAACAGAGGAGCAGCGCCGACGACGATCAGCTGGGCTTA 2627
 Db 85 CAGCAGGAGCAGCAGCAGCAGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 26
 QY 2628 CCTGAGCAGCCGC 2640
 Db 25 CAGGAGCAGCAGC 13

RESULT 40
 AX039517/c AX039517 98 bp DNA linear PAT 18-NOV-2000
 LOCUS
 DEFINITION Sequence 9 from Patent WO0063374.
 ACCESSION AX039517
 VERSION AX039517.1 GI:11229544
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 98)
 AUTHORS Lawson,A.D. and Finney,H.M.
 TITLE Synthetic transmembrane components
 JOURNAL Patent: WO 0063374-A 9 26-OCT-2000;
 CELLTECH THERAPEUTICS LIMITED (GB)
 FEATURES
 source 1..98
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="B6463"

BASE COUNT 2 a 37 c 25 g 34 t
 ORIGIN

Query Match 0.5%; Score 25; DB 6; Length 98;
 Best Local Similarity 58.9%; Pred. No. 2.2e+06;
 Matches 43; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2568 CACTATGCTGAACATGCTCAACAGAGGAGCAGCGCCGACGACGATCAGCTGGGCTTA 2627
 Db 85 CAGCAGGAGCAGCAGCAGCAGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 26
 QY 2628 CCTGAGCAGCCGC 2640
 Db 25 CAGGAGCAGCAGC 13

Search completed: December 11, 2002, 05:01:57
 Job time : 8401 secs

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 00:29:46 ; Search time 638 Seconds

(without alignments)
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Title: US-09-910-185-3

Perfect score: 5055
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	60	1.2	60	24	ABN34264 Human
2	55.4	1.1	65	24	ABN52341 Mouse spliced tran
3	31	0.6	31	22	AA130935 Human single nucle
4	31	0.6	31	22	AA130936 Human single nucle
5	29.6	0.6	78	19	AAV17231 SCA2 gene CAG repe
6	28	0.6	69	19	AAV17234 SCA2 gene CAG repe
7	28	0.6	78	19	AAV17232 SCA2 gene CAG repe
8	28	0.6	78	19	AAV17233 SCA2 gene CAG repe
9	28	0.6	88	22	AA65409 Oligonucleotide B6

10	27.6	0.5	75	22	AA513081 DNA encoding zinc
11	27.6	0.5	90	24	ABK36865 Human DNA encoding
12	27.6	0.5	95	21	AAA97078 G5 synthetic gene
13	27.4	0.5	99	17	AA727118 Hepatitis E virus
14	27.4	0.5	99	18	AA196968 Hepatitis E virus
15	26.8	0.5	51	22	AA128393 Human SNP oligonuc
16	26.8	0.5	51	22	AA128394 Human SNP oligonuc
17	26.4	0.5	75	19	AAV17230 SCA2 gene CAG repe
18	26.2	0.5	51	22	AA126912 Human SNP oligonuc
19	26.2	0.5	89	19	AA68382 Human SNP oligonuc
20	26.2	0.5	90	20	AA53913 Human tryptase-I a
21	26.2	0.5	90	21	AA19478 Human tryptase-I p
22	26.2	0.5	90	21	AAA33356 Low adenosine anti
23	26	0.5	66	18	AA78908 Poly-glutamine rep
24	26	0.5	86	22	AA65408 Oligonucleotide B6
25	25.8	0.5	41	22	AAH73705 Human zinc finger
26	25.8	0.5	65	24	ABN52286 Mouse spliced tran
27	25.8	0.5	74	24	AAAD24301 der 22 DNA related
28	25.8	0.5	84	21	AAAC21832 Human secreted pro
29	25.8	0.5	97	21	AAA36669 RSV and PIV fusion
30	25.6	0.5	60	24	ABN36458 Human spliced tran
31	25.6	0.5	17	AA733692 Nucleic acid encod	
32	25.6	0.5	92	18	AAV05454 DNA for immunodu
33	25.6	0.5	93	18	AAV00492 DNA for immunodu
34	25.6	0.5	93	18	AAV05448 DNA for immunodu
35	25.6	0.5	93	18	AAV05449 DNA for immunodu
36	25.6	0.5	93	18	AAV05458 DNA for immunodu
37	25.6	0.5	93	18	AAV05459 DNA for immunodu
38	25.6	0.5	96	18	AAV05456 DNA for immunodu
39	25.6	0.5	96	24	ABK43215 Recombinant adeny
40	25.6	0.5	98	22	AAAT20331 Human foetal liver
41	25.6	0.5	98	22	ABK72757 Human brain expres
42	25.6	0.5	98	22	AA152743 Human bone marrow
43	25.6	0.5	98	22	AA152743 Human bone marrow
44	25.4	0.5	60	24	ABN33803 Human spliced tran
45	25.4	0.5	63	15	AAQ57443 D-3-phosphoglycer
46	25.4	0.5	86	21	AAAC10510 Human secreted pro
47	25.4	0.5	90	18	AAAT76105 Human tryptase-I a
48	25.4	0.5	99	21	AAZ32898 Streptococcus pyog
49	25.2	0.5	50	22	AA128392 Human SNP oligonuc
50	25.2	0.5	51	22	AA127313 Human SNP oligonuc
51	25.2	0.5	65	24	ABN27846 Rat spliced transcr
52	25.2	0.5	83	22	ABA69965 Human foetal liver
53	25.2	0.5	83	22	ABA69965 Human foetal liver
54	25.2	0.5	83	22	AAK18174 Human brain expres
55	25.2	0.5	83	22	AAK44067 Human bone marrow
56	25.2	0.5	83	22	AA150077 Human bone marrow
57	25.2	0.5	83	24	ABN18300 Human genome-deriv
58	25.2	0.5	86	21	ABL50869 Modified erythrocy
59	25.2	0.5	94	21	AAZ43764 Human PCR derived
60	25	0.5	25	24	ABT03608 Human GIL-3 gene p
61	25	0.5	98	22	AA65404 Oligonucleotide B6
62	25	0.5	100	22	AA65405 Oligonucleotide B6
63	24.8	0.5	50	22	AA128390 Human SNP oligonuc
64	24.8	0.5	50	22	AA128391 Human SNP oligonuc
65	24.8	0.5	77	22	AA65410 Human SNP oligonuc
66	24.8	0.5	79	22	ABA70065 Human foetal liver
67	24.8	0.5	79	22	ABA36864 Human brain expres
68	24.8	0.5	79	22	AAK18276 Human brain expres
69	24.8	0.5	79	22	AAK44174 Human bone marrow
70	24.8	0.5	79	22	AA150181 Human genome-deriv
71	24.8	0.5	79	22	AA65411 Oligonucleotide B6
72	24.8	0.5	79	22	ABN18409 Human genome-deriv
73	24.8	0.5	84	15	AAQ54074 DNA encoding a dom
74	24.8	0.5	86	22	AA65408 Oligonucleotide B6
75	24.8	0.5	88	22	AA65409 Oligonucleotide B6
76	24.8	0.5	91	21	AAAC15751 Human secreted pro
77	24.8	0.5	92	22	AA65406 Oligonucleotide B6
78	24.8	0.5	94	22	AA65407 Oligonucleotide B6
79	24.8	0.5	98	22	AA65404 Oligonucleotide B6
80	24.8	0.5	100	22	AA65405 Oligonucleotide B6
81	24.6	0.5	54	24	ABN5896 Oligonucleotide B6
82	24.6	0.5	62	21	AAAC12223 Human secreted pro

C 83	24.6	0.5	92	22	AAC65406	Oligonucleotide B6	156	23.8	0.5	99	22	AAH76169	Plasmid pAMV4 co
C 84	24.6	0.5	94	22	AAC65407	Oligonucleotide B6	157	23.8	0.5	100	17	AAH76169	Primer 32 for 95 k
C 85	24.6	0.5	97	21	AAK05644	Oligonucleotide SE	158	23.6	0.5	51	22	AAH76169	Human SNP oligonuc
C 86	24.6	0.5	100	22	AAK05647	Human bone marrow	159	23.6	0.5	65	24	AAH76169	Mouse spliced tran
C 87	24.6	0.5	100	22	ABS20925	Human genome-deriv	160	23.6	0.5	79	20	AAH76169	Trypsin inhibitor
C 88	24.4	0.5	50	22	AAL34109	Human SNP oligonuc	161	23.6	0.5	80	19	AAH76169	Oligonucleotide se
C 89	24.4	0.5	81	22	AAD11241	91-fl primer used	162	23.6	0.5	80	24	AAH76169	OST311 related ol
C 90	24.4	0.5	87	24	AAD30431	29 mer oligonucleo	163	23.6	0.5	90	24	AAH76169	Human DNA encoding
C 91	24.4	0.5	90	24	ABK36835	Human DNA encoding	164	23.6	0.5	98	22	AAH76169	Human breast cell
C 92	24.4	0.5	94	15	AAQ44720	Oligonucleotide us	165	23.6	0.5	98	22	AAH76169	Human breast cell
C 93	24.4	0.5	96	15	ABA17038	Human nervous syst	166	23.6	0.5	98	22	AAH76169	Human foetal liver
C 94	24.4	0.5	96	22	ABA08157	Human ovarian and	167	23.6	0.5	98	22	AAH76169	Human foetal liver
C 95	24.4	0.5	96	22	AA829165	Genomic sequence #	168	23.6	0.5	98	22	AAH76169	Human foetal liver
C 96	24.4	0.5	96	22	AAL07123	Human reproductive	169	23.6	0.5	98	22	AAH76169	Human foetal liver
C 97	24.4	0.5	96	22	AAK73938	Human immune/haema	170	23.6	0.5	98	22	AAH76169	Probe #10402 for g
C 98	24.4	0.5	96	22	AAK89377	Human digestive sy	171	23.6	0.5	98	22	AAH76169	Probe #11898 for g
C 99	24.4	0.5	97	24	ABN65907	Human cancer relat	172	23.6	0.5	98	22	AAH76169	Probe #14917 for g
C 100	24.2	0.5	41	22	AAH73706	Human zinc finger	173	23.6	0.5	98	22	AAH76169	Human brain expres
C 101	24.2	0.5	50	22	AAL28998	Human SNP oligonuc	174	23.6	0.5	98	22	AAH76169	Human brain expres
C 102	24.2	0.5	57	19	AAV17235	SCA2 gene CAG repe	175	23.6	0.5	98	22	AAH76169	Human bone marrow
C 103	24.2	0.5	60	24	ABN43593	Human spliced tran	176	23.6	0.5	98	22	AAH76169	Human bone marrow
C 104	24.2	0.5	61	22	AAK32488	Human CB38 exon 1	177	23.6	0.5	98	22	AAH76169	Probe #9725 for ge
C 105	24.2	0.5	69	15	AAQ54075	DNA encoding a bom	178	23.6	0.5	98	22	AAH76169	Probe #11220 for g
C 106	24.2	0.5	81	18	AAH76102	Human beta tryptas	179	23.6	0.5	98	22	AAH76169	Probe #13673 used
C 107	24.2	0.5	81	20	AAK53910	Human beta tryptas	180	23.6	0.5	98	22	AAH76169	Probe #15249 used
C 108	24.2	0.5	81	21	AAH76102	Human beta tryptas	181	23.6	0.5	98	22	AAH76169	Probe #18338 used
C 109	24.2	0.5	81	21	AAH76102	Human beta tryptas	182	23.6	0.5	98	22	AAH76169	Probe #5500 used t
C 110	24.2	0.5	87	22	ABA69608	Low adenosine anti	183	23.6	0.5	98	22	AAH76169	Probe #5982 used t
C 111	24.2	0.5	87	22	AAH76102	Human foetal liver	184	23.6	0.5	98	22	AAH76169	Probe #9912 used t
C 112	24.2	0.5	87	22	AAI24439	Probe #14372 for g	185	23.6	0.5	98	22	AAH76169	Human genome-deriv
C 113	24.2	0.5	87	22	ABSI17852	Human genome-deriv	186	23.6	0.5	98	22	AAH76169	Human genome-deriv
C 114	24.2	0.5	90	24	ABK17248	Coupled ligation a	187	23.6	0.5	98	22	AAH76169	Human genome-deriv
C 115	24.2	0.5	90	24	ABK17293	Coupled ligation a	188	23.6	0.5	98	22	AAH76169	Human foetal liver
C 116	24.2	0.5	94	22	AAH76102	Codon-optimised HP	189	23.6	0.5	98	22	AAH76169	Probe #18813 for g
C 117	24.2	0.5	94	22	AAH76102	Hepatitis E virus	190	23.6	0.5	98	22	AAH76169	Human bone marrow
C 118	24.2	0.5	99	18	AAH76102	Hepatitis E virus	191	23.6	0.5	98	22	AAH76169	Probe #17397 for g
C 119	24.2	0.5	99	18	AAH76102	Codon-optimised HP	192	23.6	0.5	98	22	AAH76169	Probe #25119 used
C 120	24.2	0.5	100	24	ABK180050	Human ovarian canc	193	23.4	0.5	60	24	AAH76169	Human genome-deriv
C 121	24.2	0.5	100	24	ABK180050	Human ovarian canc	194	23.4	0.5	62	21	AAH76169	Human spliced tran
C 122	24.2	0.5	72	17	AAH76102	Human GIL-3 gene p	195	23.4	0.5	66	21	AAH76169	Polydr adaptor use
C 123	24.2	0.5	72	17	AAH76102	VDJ joint sequence	196	23.4	0.5	71	20	AAH76169	Human cancer assoc
C 124	24.2	0.5	80	21	ABK12554	VDH21 Dp 1 mu clo	197	23.4	0.5	75	17	AAH76169	Murine homeobox HO
C 125	24.2	0.5	84	17	AAH76102	Modified erythro	198	23.4	0.5	77	17	AAH76169	VDJ joint sequence
C 126	24.2	0.5	84	17	AAH76102	Nucleic acid encod	199	23.4	0.5	77	17	AAH76169	VDH21 DHQ52 J4 mu
C 127	24.2	0.5	84	17	AAH76102	Nucleic acid encod	200	23.4	0.5	77	17	AAH76169	VDJ joint sequence
C 128	24.2	0.5	87	15	AAH76102	Oligonucleotide us	201	23.4	0.5	77	22	AAH76169	VDH21 DIR2 J4 mu c
C 129	24.2	0.5	87	20	AAH76102	Oligonucleotide C2	202	23.4	0.5	78	19	AAH76169	Oligonucleotide B6
C 130	24.2	0.5	91	22	AAH76102	dCMP-specific apta	203	23.4	0.5	79	22	AAH76169	Oligonucleotide SE
C 131	24.2	0.5	97	24	AAH76102	Synthetic Env poly	204	23.4	0.5	80	17	AAH76169	VDJ joint sequence
C 132	24.2	0.5	100	15	AAH76102	Candida albicans-s	205	23.4	0.5	80	18	AAH76169	VDH21 DXP1 J4 mu c
C 133	24.2	0.5	100	15	AAH76102	Candida albicans-s	206	23.4	0.5	81	17	AAH76169	VDJ joint sequence
C 134	24.2	0.5	100	18	AAH76102	Human IL4 receptor	207	23.4	0.5	81	18	AAH76169	VDH21 DIR2 J4 mu c
C 135	24.2	0.5	100	18	AAH76102	Human IL4 receptor	208	23.4	0.5	81	17	AAH76169	VDJ joint sequence
C 136	24.2	0.5	100	21	AAH76102	Human IL4 receptor	209	23.4	0.5	84	17	AAH76169	VDJ joint sequence
C 137	24.2	0.5	100	21	AAH76102	Low adenosine anti	210	23.4	0.5	84	18	AAH76169	VDH21 DHQ52 J4 mu c
C 138	24.2	0.5	100	21	AAH76102	Human Fas ligand g	211	23.4	0.5	84	18	AAH76169	VDH21 DXP1 J4 mu c
C 139	24.2	0.5	100	21	AAH76102	Human spliced tran	212	23.4	0.5	85	17	AAH76169	VDJ joint sequence
C 140	24.2	0.5	60	24	AAH76102	Human spliced tran	213	23.4	0.5	85	18	AAH76169	VDH21 DNP1 J4 mu c
C 141	24.2	0.5	61	20	AAH76102	Complement system	214	23.4	0.5	87	17	AAH76169	VDJ joint sequence
C 142	24.2	0.5	65	24	AAH76102	Rat spliced tran	215	23.4	0.5	87	18	AAH76169	VDH21 DNP1 J4 mu c
C 143	24.2	0.5	65	24	AAH76102	Mouse spliced tran	216	23.4	0.5	89	19	AAH76169	VDH21 DNP1 J4 mu c
C 144	24.2	0.5	73	21	AAH76102	Human secreted pro	217	23.4	0.5	90	16	AAH76169	VDH21 DNP1 J4 mu c
C 145	24.2	0.5	81	18	AAH76102	Human beta tryptas	218	23.4	0.5	90	16	AAH76169	Oligonucleotide P4
C 146	24.2	0.5	81	21	AAH76102	Human beta tryptas	219	23.4	0.5	92	18	AAH76169	Codon-optimised HP
C 147	24.2	0.5	81	21	AAH76102	Human beta tryptas	220	23.4	0.5	93	18	AAH76169	VDH21 DNP1 J4 mu c
C 148	24.2	0.5	81	21	AAH76102	Low adenosine anti	221	23.4	0.5	95	19	AAH76169	HSV-1 latency asso
C 149	24.2	0.5	82	19	AAH76102	Oligonucleotide SE	222	23.4	0.5	96	21	AAH76169	Exemplary quadripl
C 150	24.2	0.5	90	19	AAH76102	Self-complementary	223	23.4	0.5	96	22	AAH76169	Human foetal liver
C 151	24.2	0.5	90	19	AAH76102	Vector PROCOM5/3 i	224	23.4	0.5	96	22	AAH76169	Human brain expres
C 152	24.2	0.5	94	19	AAH76102	HCV DNA encoding H	225	23.4	0.5	96	22	AAH76169	Human bone marrow
C 153	24.2	0.5	94	19	AAH76102	Human calcium chan	226	23.4	0.5	96	22	AAH76169	Probe #11966 used
C 154	24.2	0.5	94	21	AAH76102	HSV and PIV fusion	227	23.4	0.5	98	22	AAH76169	Human genome-deriv
C 155	24.2	0.5	94	22	AAH76102	Human EST H55223	228	23.4	0.5	98	22	AAH76169	Human angiotensino
			96	21	AAH76102	Oligonucleotide ON				100	24	AAH76169	Endothelin-2 (EDN

229	23.2	0.5	51	22	AAI78742	Human silent SNP c	302	22.8	0.5	65	24	ABN27731	Rat spliced transc
230	23.2	0.5	51	22	AAI78743	Human silent SNP c	303	22.8	0.5	65	24	ABN27855	Rat spliced transc
231	23.2	0.5	51	22	AAI78743	Human silent SNP c	304	22.8	0.5	65	24	ABN27855	Mouse spliced trans
232	23.2	0.5	72	24	ABL51932	Reverse assembly r	305	22.8	0.5	69	23	ABL53319	Artificial secreto
233	23.2	0.5	79	24	ABL50622	OST311N related ol	306	22.8	0.5	76	14	AAQ42273	PCR primer RNA-76
234	23.2	0.5	81	17	AAI88564	Secretory phosphol	307	22.8	0.5	76	16	AAQ76142	Fd gene 3' (consta
235	23.2	0.5	82	14	AAI88564	Probe (v) used in	308	22.8	0.5	76	16	AAQ92350	Human secreted pro
236	23.2	0.5	83	19	AAI88564	Probe (v) used in	309	22.8	0.5	81	21	AAI88564	Oligonucleotide se
237	23.2	0.5	83	19	AAI88564	Probe (v) used in	310	22.8	0.5	82	21	AAI88564	Oligonucleotide se
238	23.2	0.5	83	19	AAI88564	Probe (v) used in	311	22.8	0.5	82	21	AAI88564	Oligonucleotide se
239	23.2	0.5	90	22	AAH84353	Human cell death p	312	22.8	0.5	85	21	AAI88564	Oligonucleotide NR
240	23.2	0.5	90	22	AAH84353	Human cell death p	313	22.8	0.5	85	21	AAI88564	VEGF nucleic acid
241	23.2	0.5	90	22	AAH84353	Human cell death p	314	22.8	0.5	86	21	AAI88564	Modified erythro
242	23.2	0.5	90	22	AAH84353	Human cell death p	315	22.8	0.5	86	21	AAI88564	Human Ig Cmu gene
243	23.2	0.5	91	21	AAH84353	Coupled ligation a	316	22.8	0.5	87	21	AAI88564	Human secreted pro
244	23.2	0.5	91	21	AAH84353	Coupled ligation a	317	22.8	0.5	87	21	AAI88564	Oligonucleotide se
245	23.2	0.5	92	16	AAH84353	Il reverse gene co	318	22.8	0.5	90	20	AAI88564	Oligonucleotide se
246	23.2	0.5	92	16	AAH84353	Human secreted pro	319	22.8	0.5	90	21	AAI88564	Human tryptase-I a
247	23.2	0.5	93	16	AAH84353	Padlock probe alph	320	22.8	0.5	90	21	AAI88564	Human tryptase-I p
248	23.2	0.5	94	21	AAH84353	M13 bacteriophage	321	22.8	0.5	90	21	AAI88564	Low adenosine anti
249	23.2	0.5	94	21	AAH84353	Human secreted pro	322	22.8	0.5	91	22	AAI88564	Human brain expres
250	23.2	0.5	98	23	AAH84353	Oligonucleotide pr	323	22.8	0.5	91	22	AAI88564	Human bone marrow
251	23.2	0.5	98	23	AAH84353	Pseudomonas aerugi	324	22.8	0.5	91	22	AAI88564	Probe #20064 used
252	23.2	0.5	60	24	ABN14999	Human spliced tran	325	22.8	0.5	95	22	AAI88564	Human genome-deriv
253	23.2	0.5	65	21	AAI14733	Human secreted pro	326	22.8	0.5	96	22	AAI88564	Probe #10. Uniden
254	23.2	0.5	65	21	AAI14733	Human secreted pro	327	22.8	0.5	96	22	AAI88564	Arabidopsis thalia
255	23.2	0.5	65	21	AAI14733	Human secreted pro	328	22.8	0.5	97	22	AAI88564	Human foetal liver
256	23.2	0.5	65	21	AAI14733	Human secreted pro	329	22.8	0.5	97	22	AAI88564	Human brain expres
257	23.2	0.5	78	24	ABN52513	Mouse spliced tran	330	22.8	0.5	97	22	AAI88564	Human bone marrow
258	23.2	0.5	82	15	AAO44724	PCR primer 6, used	331	22.8	0.5	97	22	AAI88564	Probe #18904 used
259	23.2	0.5	82	15	AAO44724	Oligonucleotide C2	332	22.8	0.5	97	22	AAI88564	Pseudomonas aerugi
260	23.2	0.5	83	20	AAI60633	Probe #6. Uniden	333	22.8	0.5	97	22	AAI88564	Human genome-deriv
261	23.2	0.5	83	20	AAI60633	Probe #6. Uniden	334	22.8	0.5	97	22	AAI88564	Human secreted pro
262	23.2	0.5	85	19	AAV32418	Human cDNA clone B	335	22.8	0.5	99	21	AAI88564	Human immune/haema
263	23.2	0.5	85	19	AAV32418	Human cDNA clone B	336	22.8	0.5	99	21	AAI88564	Human zinc finger
264	23.2	0.5	89	21	AAV68382	Clone #8 fragment	337	22.8	0.5	41	22	AAI88564	Human GZF gene rel
265	23.2	0.5	89	21	AAV68382	Human MN gene intr	338	22.8	0.5	41	22	AAI88564	Human zinc finger
266	23.2	0.5	89	21	AAV68382	Human MN gene intr	339	22.8	0.5	41	22	AAI88564	Human spliced tran
267	23.2	0.5	89	21	AAV68382	Human MN gene intr	340	22.8	0.5	41	22	AAI88564	Human spliced tran
268	23.2	0.5	89	21	AAV68382	Human MN gene intr	341	22.8	0.5	41	22	AAI88564	Human spliced tran
269	23.2	0.5	89	21	AAV68382	Human MN gene intr	342	22.8	0.5	41	22	AAI88564	Human spliced tran
270	23.2	0.5	89	21	AAV68382	Human MN gene intr	343	22.8	0.5	41	22	AAI88564	Human spliced tran
271	23.2	0.5	95	21	AAI17327	Codon-optimised HP	344	22.8	0.5	60	24	ABN56400	Mouse spliced tran
272	23.2	0.5	95	21	AAI17327	Codon-optimised HP	345	22.8	0.5	60	24	ABN56400	Human spliced tran
273	23.2	0.5	95	21	AAI17327	Codon-optimised HP	346	22.8	0.5	60	24	ABN56400	Human spliced tran
274	23.2	0.5	95	21	AAI17327	Codon-optimised HP	347	22.8	0.5	60	24	ABN56400	Human spliced tran
275	23.2	0.5	95	21	AAI17327	Codon-optimised HP	348	22.8	0.5	60	24	ABN56400	Human spliced tran
276	23.2	0.5	95	21	AAI17327	Codon-optimised HP	349	22.8	0.5	60	24	ABN56400	Human spliced tran
277	23.2	0.5	95	21	AAI17327	Codon-optimised HP	350	22.8	0.5	60	24	ABN56400	Human spliced tran
278	23.2	0.5	95	21	AAI17327	Codon-optimised HP	351	22.8	0.5	60	24	ABN56400	Human spliced tran
279	23.2	0.5	95	21	AAI17327	Codon-optimised HP	352	22.8	0.5	60	24	ABN56400	Human spliced tran
280	23.2	0.5	95	21	AAI17327	Codon-optimised HP	353	22.8	0.5	60	24	ABN56400	Human spliced tran
281	23.2	0.5	95	21	AAI17327	Codon-optimised HP	354	22.8	0.5	60	24	ABN56400	Human spliced tran
282	23.2	0.5	95	21	AAI17327	Codon-optimised HP	355	22.8	0.5	60	24	ABN56400	Human spliced tran
283	23.2	0.5	95	21	AAI17327	Codon-optimised HP	356	22.8	0.5	60	24	ABN56400	Human spliced tran
284	23.2	0.5	95	21	AAI17327	Codon-optimised HP	357	22.8	0.5	60	24	ABN56400	Human spliced tran
285	23.2	0.5	95	21	AAI17327	Codon-optimised HP	358	22.8	0.5	60	24	ABN56400	Human spliced tran
286	23.2	0.5	95	21	AAI17327	Codon-optimised HP	359	22.8	0.5	60	24	ABN56400	Human spliced tran
287	23.2	0.5	95	21	AAI17327	Codon-optimised HP	360	22.8	0.5	60	24	ABN56400	Human spliced tran
288	23.2	0.5	95	21	AAI17327	Codon-optimised HP	361	22.8	0.5	60	24	ABN56400	Human spliced tran
289	23.2	0.5	95	21	AAI17327	Codon-optimised HP	362	22.8	0.5	60	24	ABN56400	Human spliced tran
290	23.2	0.5	95	21	AAI17327	Codon-optimised HP	363	22.8	0.5	60	24	ABN56400	Human spliced tran
291	23.2	0.5	95	21	AAI17327	Codon-optimised HP	364	22.8	0.5	60	24	ABN56400	Human spliced tran
292	23.2	0.5	95	21	AAI17327	Codon-optimised HP	365	22.8	0.5	60	24	ABN56400	Human spliced tran
293	23.2	0.5	95	21	AAI17327	Codon-optimised HP	366	22.8	0.5	60	24	ABN56400	Human spliced tran
294	23.2	0.5	95	21	AAI17327	Codon-optimised HP	367	22.8	0.5	60	24	ABN56400	Human spliced tran
295	23.2	0.5	95	21	AAI17327	Codon-optimised HP	368	22.8	0.5	60	24	ABN56400	Human spliced tran
296	23.2	0.5	95	21	AAI17327	Codon-optimised HP	369	22.8	0.5	60	24	ABN56400	Human spliced tran
297	23.2	0.5	95	21	AAI17327	Codon-optimised HP	370	22.8	0.5	60	24	ABN56400	Human spliced tran
298	23.2	0.5	95	21	AAI17327	Codon-optimised HP	371	22.8	0.5	60	24	ABN56400	Human spliced tran
299	23.2	0.5	95	21	AAI17327	Codon-optimised HP	372	22.8	0.5	60	24	ABN56400	Human spliced tran
300	23.2	0.5	95	21	AAI17327	Codon-optimised HP	373	22.8	0.5	60	24	ABN56400	Human spliced tran
301	23.2	0.5	95	21	AAI17327	Codon-optimised HP	374	22.8	0.5	60	24	ABN56400	Human spliced tran

C 375	22.6	0.4	96	16	AAO98885	Anti-human IL-4 MA	C 448	22.2	0.4	60	18	AA772229	Fibroblast growth
C 376	22.6	0.4	97	19	AAV81329	Oligonucleotide HL	C 449	22.2	0.4	60	24	ABN33575	Human spliced tran
C 377	22.6	0.4	97	19	AAV81323	Oligonucleotide HL	C 450	22.2	0.4	60	24	ABN33575	Human spliced tran
C 378	22.6	0.4	97	22	AAH74751	Oligonucleotide US	C 451	22.2	0.4	60	24	ABN50897	Human spliced tran
C 379	22.6	0.4	97	22	AAH74757	Oligonucleotide US	C 452	22.2	0.4	60	24	AAH33617	Human spliced tran
C 380	22.6	0.4	97	24	ABA95549	Oligonucleotide HL	C 453	22.2	0.4	60	24	AAH33617	Human spliced tran
C 381	22.6	0.4	97	24	ABA95555	Oligonucleotide HL	C 454	22.2	0.4	65	24	ABN51184	Mouse spliced tran
C 382	22.6	0.4	99	22	AA676699	Insulator plasmid	C 455	22.2	0.4	65	24	ABN56214	Mouse spliced tran
C 383	22.6	0.4	100	16	AAO98894	Anti-human IL-4 MA	C 456	22.2	0.4	65	24	ABN56561	Mouse spliced tran
C 384	22.6	0.4	100	16	AAO98884	Anti-human IL-4 MA	C 457	22.2	0.4	66	22	AA670599	Mouse spliced tran
C 385	22.6	0.4	100	16	ABA50227	Human breast cell	C 458	22.2	0.4	67	15	AA670599	Mouse spliced tran
C 386	22.6	0.4	100	22	ABA68172	Human foetal liver	C 459	22.2	0.4	69	22	AA670599	Mouse spliced tran
C 387	22.6	0.4	100	22	ABA58182	Probe #13648 for g	C 460	22.2	0.4	78	19	AA670599	Mouse spliced tran
C 388	22.6	0.4	100	22	AAK16547	Human brain expres	C 461	22.2	0.4	78	21	AAK13452	Human secreted pro
C 389	22.6	0.4	100	22	AAK16547	Human bone marrow	C 462	22.2	0.4	80	22	AAK13457	Human secreted pro
C 390	22.6	0.4	100	22	AAI33079	Probe #13012 for g	C 463	22.2	0.4	89	21	AAK13457	Human secreted pro
C 391	22.6	0.4	100	22	AAI48381	Probe #17067 used t	C 464	22.2	0.4	90	18	AAK13457	Human secreted pro
C 392	22.6	0.4	100	22	AAI08731	Probe #8722 used t	C 465	22.2	0.4	90	18	AAK13457	Human secreted pro
C 393	22.6	0.4	100	22	ABN16359	Human genome-deriv	C 466	22.2	0.4	90	19	AAK13457	Human secreted pro
C 394	22.6	0.4	45	22	AAO4753	Synthetic gene shp	C 467	22.2	0.4	90	20	AAK13457	Human secreted pro
C 395	22.4	0.4	51	22	AAI28996	Human SNP oligonuc	C 468	22.2	0.4	90	22	AAK54467	Human secreted pro
C 396	22.4	0.4	51	22	AAI30314	Human SNP oligonuc	C 469	22.2	0.4	91	21	AAK54467	Human secreted pro
C 397	22.4	0.4	51	22	ABK50584	Bipartite probe #7	C 470	22.2	0.4	91	21	ABN72785	Human secreted pro
C 398	22.4	0.4	54	21	AAZ49589	Downstream PCR pri	C 471	22.2	0.4	95	21	AAK16473	Human secreted pro
C 399	22.4	0.4	54	23	ABL53321	Artificial secret	C 472	22.2	0.4	99	15	AAK16473	Human secreted pro
C 400	22.4	0.4	60	24	ABN33554	Human spliced tran	C 473	22.2	0.4	100	20	AAK84414	Human secreted pro
C 401	22.4	0.4	60	24	ABN50125	Human spliced tran	C 474	22.2	0.4	100	24	ABO72751	Human secreted pro
C 402	22.4	0.4	65	24	ABN29714	Rat spliced trans	C 475	22.2	0.4	100	24	ABO72751	Human secreted pro
C 403	22.4	0.4	65	24	ABN57750	Mouse spliced tran	C 476	22.2	0.4	48	24	ABN84039	Human secreted pro
C 404	22.4	0.4	69	17	AAK73256	VDJ joint sequence	C 477	22.2	0.4	51	19	ABN84039	Human secreted pro
C 405	22.4	0.4	72	18	AAV12551	VH251 - J1 mu clon	C 478	22.2	0.4	51	22	AAK73256	Human secreted pro
C 406	22.4	0.4	72	16	AAO27114	3' PCR primer 772	C 479	22.2	0.4	51	22	AAK73256	Human secreted pro
C 407	22.4	0.4	72	16	AAO99016	Chelating peptide-	C 480	22.2	0.4	51	22	AAK73256	Human secreted pro
C 408	22.4	0.4	75	21	AAK27616	Human secreted pro	C 481	22.2	0.4	51	22	AAK73256	Human secreted pro
C 409	22.4	0.4	81	16	AAK18956	Oligonucleotide P3	C 482	22.2	0.4	51	22	AAK73256	Human secreted pro
C 410	22.4	0.4	86	24	AAK4293	Human BS135 coding	C 483	22.2	0.4	52	21	AAK12920	Human secreted pro
C 411	22.4	0.4	86	24	AAK40041	Breast tissue libr	C 484	22.2	0.4	54	22	AAK12920	Human secreted pro
C 412	22.4	0.4	89	22	AAK44433	Human beta-amyloid	C 485	22.2	0.4	55	13	AAK12920	Human secreted pro
C 413	22.4	0.4	89	22	AAK16707	gGMP-specific apta	C 486	22.2	0.4	55	16	AAK12920	Human secreted pro
C 414	22.4	0.4	93	21	ABN81024	Shrimp poly nucleot	C 487	22.2	0.4	56	20	AAK12920	Human secreted pro
C 415	22.4	0.4	93	21	AAK28554	Oligonucleotide C2	C 488	22.2	0.4	60	24	ABN35501	Human secreted pro
C 416	22.4	0.4	95	20	AAK19442	Human secreted pro	C 489	22.2	0.4	60	24	ABN35501	Human secreted pro
C 417	22.4	0.4	97	21	AAK17135	Human secreted pro	C 490	22.2	0.4	60	24	ABN35501	Human secreted pro
C 418	22.4	0.4	98	19	AAV24255	Chimeric antibody	C 491	22.2	0.4	60	24	ABN41478	Human secreted pro
C 419	22.4	0.4	98	22	AAK00100	Human antibody PCR	C 492	22.2	0.4	61	24	ABN41478	Human secreted pro
C 420	22.4	0.4	98	21	AAK58881	PCR primer H1AMB3	C 493	22.2	0.4	65	24	ABN52571	Human secreted pro
C 421	22.4	0.4	98	22	AAH75074	Nucleotide sequenc	C 494	22.2	0.4	65	24	ABN52571	Human secreted pro
C 422	22.4	0.4	98	22	AAH74255	Nucleotide sequenc	C 495	22.2	0.4	67	15	AAK29493	Human secreted pro
C 423	22.4	0.4	98	22	AAH76612	Human Ig lambda J1	C 496	22.2	0.4	72	21	AAK29493	Human secreted pro
C 424	22.4	0.4	98	22	AAK69097	Human L chain lamb	C 497	22.2	0.4	72	21	AAK29493	Human secreted pro
C 425	22.4	0.4	98	22	AAK69153	Human L chain lamb	C 498	22.2	0.4	74	20	AAK29493	Human secreted pro
C 426	22.4	0.4	98	22	AAK69209	Human L chain lamb	C 499	22.2	0.4	75	16	AAK29493	Human secreted pro
C 427	22.4	0.4	98	24	ABN73403	Bovine embryonic g	C 500	22.2	0.4	80	19	AAK29493	Human secreted pro
C 428	22.4	0.4	98	24	ABN73403	Joint disease rela	C 501	22.2	0.4	80	20	AAK29493	Human secreted pro
C 429	22.4	0.4	99	21	AAA36687	RSV and PIV fusion	C 502	22.2	0.4	81	14	AAK29493	Human secreted pro
C 430	22.4	0.4	100	17	AAK09184	Hepatitis C virus	C 503	22.2	0.4	81	20	AAK29493	Human secreted pro
C 431	22.4	0.4	100	19	AAV22776	Hepatitis C virus	C 504	22.2	0.4	81	22	AAK29493	Human secreted pro
C 432	22.4	0.4	100	19	AAV20726	Amp-probe-2 (HCV B	C 505	22.2	0.4	82	22	AAK29493	Human secreted pro
C 433	22.4	0.4	100	22	AAK60019	Hepatitis C virus	C 506	22.2	0.4	82	22	AAK29493	Human secreted pro
C 434	22.4	0.4	100	22	AAK60020	CDNA linker primer	C 507	22.2	0.4	84	17	AAK60020	Human secreted pro
C 435	22.4	0.4	100	24	ABK68846	Hepatitis C VB amp	C 508	22.2	0.4	85	22	AAK60020	Human secreted pro
C 436	22.2	0.4	47	21	AAK26784	Human map-related	C 509	22.2	0.4	85	22	AAK60020	Human secreted pro
C 437	22.2	0.4	50	22	AAI28997	Human SNP oligonuc	C 510	22.2	0.4	85	22	AAK60020	Human secreted pro
C 438	22.2	0.4	51	22	AAI77248	Human silent SNP c	C 511	22.2	0.4	85	22	AAK60020	Human secreted pro
C 439	22.2	0.4	51	22	AAH79741	Human DNA contain	C 512	22.2	0.4	85	22	AAK60020	Human secreted pro
C 440	22.2	0.4	53	18	AAV76054	Staphylococcus aur	C 513	22.2	0.4	85	22	AAK60020	Human secreted pro
C 441	22.2	0.4	53	24	ABK56941	Rabies surface gly	C 514	22.2	0.4	85	24	ABK56941	Human secreted pro
C 442	22.2	0.4	56	24	ABK54701	Human colon cancer	C 515	22.2	0.4	89	21	AAK11387	Human secreted pro
C 443	22.2	0.4	57	22	AAK74351	Repetitive protein	C 516	22.2	0.4	91	21	AAK11387	Human secreted pro
C 444	22.2	0.4	57	22	AAK74352	Repetitive protein	C 517	22.2	0.4	91	21	AAK11387	Human secreted pro
C 445	22.2	0.4	57	22	AAK74352	Oligonucleotide us	C 518	22.2	0.4	92	20	AAK23496	Human secreted pro
C 446	22.2	0.4	57	22	AAK74352	Oligonucleotide us	C 519	22.2	0.4	92	21	AAK23496	Human secreted pro
C 447	22.2	0.4	58	24	ABL32015	Apoe2150-LR target	C 520	22.2	0.4	93	22	ABK74544	Human foetal liver

c 521	22	0.4	93	22	ABA39360	Probe #17826 for g	594	21.6	0.4	60	24	ABN42468	Human spliced tran
c 522	22	0.4	93	22	AAK23011	Human brain expres	595	21.6	0.4	60	24	ABN47150	Human spliced tran
c 523	22	0.4	93	22	AAK49188	Human bone marrow	c 596	21.6	0.4	62	21	AAK12223	Human spliced tran
c 524	22	0.4	93	22	AAI26445	Probe #16378 for g	597	21.6	0.4	65	24	ABN52336	Mouse spliced tran
c 525	22	0.4	93	22	AAI55023	Probe #23709 used	598	21.6	0.4	65	24	ABN53216	Mouse spliced tran
c 526	22	0.4	93	24	ABN22756	Human genome-deriv	c 599	21.6	0.4	65	24	ABN56112	Mouse spliced tran
c 527	22	0.4	96	22	AAK89782	Human digestive sy	c 600	21.6	0.4	65	24	ABN56830	Mouse spliced tran
c 528	22	0.4	96	22	AAK89785	Human digestive sy	c 601	21.6	0.4	68	20	AAK25127	Mouse spliced tran
c 529	22	0.4	97	21	AAK18714	Human secreted pro	c 602	21.6	0.4	69	20	AAK86081	PCR primer used to
c 530	22	0.4	99	21	AAK14673	Nucleotide sequenc	c 603	21.6	0.4	69	20	AAK60513	W09914235 seq ID N
c 531	22	0.4	99	22	AAI54496	Probe #23182 used	c 604	21.6	0.4	70	24	ABK16426	Ashb2a gossypii ge
c 532	22	0.4	100	21	AAK11867	Human secreted pro	c 605	21.6	0.4	71	20	AAK207015	Murine alpha-L-idu
c 533	21.8	0.4	50	22	AAI28314	Human SNP oligonuc	c 606	21.6	0.4	72	21	AAK69994	Human ovarian carc
c 534	21.8	0.4	50	22	AAI31324	Human SNP oligonuc	c 607	21.6	0.4	72	24	ABN72888	Ovarian carcinoma
c 535	21.8	0.4	51	22	AAI26920	Human SNP oligonuc	c 608	21.6	0.4	73	21	AAK12579	Synthetic DNA enco
c 536	21.8	0.4	51	22	AAI29554	Human SNP oligonuc	c 609	21.6	0.4	75	21	AAK11406	Human secreted pro
c 537	21.8	0.4	60	21	AAK29503	Codon altered alfa	c 610	21.6	0.4	75	22	AAK90518	Human secreted pro
c 538	21.8	0.4	60	24	ABN38638	Human spliced tran	c 611	21.6	0.4	76	22	AAK04557	PCR primer for mou
c 539	21.8	0.4	60	24	ABN40018	Human spliced tran	c 612	21.6	0.4	81	17	AAK15843	BPI potentiating p
c 540	21.8	0.4	60	24	ABN47632	Human spliced tran	c 613	21.6	0.4	82	21	AAK12514	Oligonucleotide us
c 541	21.8	0.4	60	24	AAK07154	PV37A-LTR oligonuc	c 614	21.6	0.4	82	23	ABV35219	Human prostate exp
c 542	21.8	0.4	65	24	ABN31635	Rat spliced trans	c 615	21.6	0.4	83	20	AAK19771	Porcine adenovirus
c 543	21.8	0.4	65	24	ABN54406	Mouse spliced tran	c 616	21.6	0.4	84	16	AAK22835	Human gene signatu
c 544	21.8	0.4	65	24	ABN57609	Mouse spliced tran	c 617	21.6	0.4	84	12	AAK21972	Human collagen gen
c 545	21.8	0.4	65	24	ABN58348	Mouse spliced tran	c 618	21.6	0.4	85	15	AAK074761	Human prepro-eryth
c 546	21.8	0.4	65	24	ABN58357	Mouse spliced tran	c 619	21.6	0.4	85	22	ABK74482	Human foetal liver
c 547	21.8	0.4	67	15	AAK06017	COL2A1 5' primer (c 620	21.6	0.4	85	22	ABK39326	Probe #17792 for g
c 548	21.8	0.4	68	18	AAV79231	Staphylococcus aur	c 621	21.6	0.4	85	22	AAK22949	Human brain expres
c 549	21.8	0.4	69	15	AAK063712	Synthetic 2S seed	c 622	21.6	0.4	85	22	AAK49123	Human bone marrow
c 550	21.8	0.4	70	20	AAK20584	CTLA-4 variable 11	c 623	21.6	0.4	85	22	AAI54953	Probe #23639 used
c 551	21.8	0.4	75	17	AAK42304	Probe sequence whl	c 624	21.6	0.4	85	24	ABK22708	Human genome-deriv
c 552	21.8	0.4	75	20	AAK78126	HLA-B/HLA-E chim	c 625	21.6	0.4	87	21	AAK55942	Reverse oligonucle
c 553	21.8	0.4	75	22	AAK13077	DNA encoding zinc	c 626	21.6	0.4	87	21	AAK55944	Forward oligonucle
c 554	21.8	0.4	78	19	AAK11626	Human secreted pro	c 627	21.6	0.4	87	24	AAK31516	PCK primer 7, used
c 555	21.8	0.4	83	19	AAK22180	Oligonucleotide se	c 628	21.6	0.4	90	22	AAK07235	P. tititici Tox21A/
c 556	21.8	0.4	83	21	AAK88283	EBST gene constuc	c 629	21.6	0.4	90	24	ABK76766	Bacillus lichenif
c 557	21.8	0.4	84	23	AAK47902	Enterococcus faeca	c 630	21.6	0.4	90	24	ABK36412	HIV DNA encoding G
c 558	21.8	0.4	87	22	ABK71258	Human foetal liver	c 631	21.6	0.4	90	24	ABK36780	Human DNA encoding
c 559	21.8	0.4	87	22	ABK37556	Probe #16022 for g	c 632	21.6	0.4	90	24	ABK82732	Human protective D
c 560	21.8	0.4	87	22	AAK19559	Human brain expres	c 633	21.6	0.4	93	9	AAK81186	Synthetic DNA sequ
c 561	21.8	0.4	87	22	AAK45556	Human bone marrow	c 634	21.6	0.4	94	24	ABK91737	DNA encoding murin
c 562	21.8	0.4	87	22	AAI25320	Probe #15253 for g	c 635	21.6	0.4	95	22	ABK50050	Human breast cell
c 563	21.8	0.4	87	22	AAI51496	Probe #20182 used	c 636	21.6	0.4	95	22	ABK67982	Human foetal liver
c 564	21.8	0.4	87	24	ABK19826	Human genome-deriv	c 637	21.6	0.4	95	22	AAK16375	Human brain expres
c 565	21.8	0.4	89	19	AAK64896	HSV-1 latency asso	c 638	21.6	0.4	95	22	AAK42126	Human bone marrow
c 566	21.8	0.4	89	22	AAK24137	Human brain expres	c 639	21.6	0.4	95	22	AAI48190	Probe #16876 used
c 567	21.8	0.4	89	22	AAI56135	Probe #24821 used	c 640	21.6	0.4	95	24	ABK16170	Human genome-deriv
c 568	21.8	0.4	89	22	AAK65421	Oligonucleotide A8	c 641	21.6	0.4	95	24	ABK11007	Oligonucleotide MN
c 569	21.8	0.4	90	24	ABK36558	HCV DNA encoding H	c 642	21.6	0.4	97	24	AAI71078	Humanised Proder P
c 570	21.8	0.4	91	12	AAK65420	Oligonucleotide A8	c 643	21.6	0.4	99	21	AAK36736	MV and MV fusion
c 571	21.8	0.4	93	17	AAK73258	VDJ joint sequence	c 644	21.6	0.4	100	22	AAK46402	Oligonucleotide c1
c 572	21.8	0.4	93	21	AAK29660	DNA coding for the	c 645	21.4	0.4	49	22	AAI79263	Human silent SNP c
c 573	21.8	0.4	95	19	AAK64889	HSV-1 latency asso	c 646	21.4	0.4	55	22	AAH73846	Thermal amplificat
c 574	21.8	0.4	95	21	AAK87736	Anti-human VEGF re	c 647	21.4	0.4	60	20	AAK36603	Mammalian CERP imm
c 575	21.8	0.4	95	22	AAK70213	Anti-human FLT-1 a	c 648	21.4	0.4	60	22	AAK89452	Human genetic mark
c 576	21.8	0.4	95	24	ABK11007	Oligonucleotide MN	c 649	21.4	0.4	60	24	ABK31119	Human spliced tran
c 577	21.8	0.4	97	19	AAK17076	Oligonucleotide 4	c 650	21.4	0.4	60	24	ABK39655	Human spliced tran
c 578	21.8	0.4	97	21	AAK15576	Human secreted pro	c 651	21.4	0.4	60	24	ABK41305	Human spliced tran
c 579	21.8	0.4	98	21	AAK13297	Human secreted pro	c 652	21.4	0.4	60	24	ABK43680	Human spliced tran
c 580	21.8	0.4	99	16	AAK26834	Human gene signatu	c 653	21.4	0.4	60	24	ABK49744	Human spliced tran
c 581	21.8	0.4	99	18	AAK91300	Human M97-2 secret	c 654	21.4	0.4	60	24	ABK50717	Human spliced tran
c 582	21.6	0.4	47	20	AAK16201	Serine protease in	c 655	21.4	0.4	60	24	ABK59239	Human spliced tran
c 583	21.6	0.4	47	21	AAK97539	Primer used in pro	c 656	21.4	0.4	60	24	ABK59362	Human spliced tran
c 584	21.6	0.4	47	22	AAI67501	Serine protease in	c 657	21.4	0.4	62	14	AAK037291	Oligomer SM 112 us
c 585	21.6	0.4	47	23	AAH88666	CNS disorder-relat	c 658	21.4	0.4	62	16	AAK095011	PKSsg4 oligonucle
c 586	21.6	0.4	50	22	AAI34154	Human SNP oligonuc	c 659	21.4	0.4	62	20	AAK30476	Oligonucleotide fo
c 587	21.6	0.4	51	19	AAK28951	Plasmid pAMG21 hfg	c 660	21.4	0.4	62	20	AAK93616	Oligonucleotide SE
c 588	21.6	0.4	59	12	AAH9165	Escherichia coli B	c 661	21.4	0.4	62	21	AAK13823	Oligonucleotide #1
c 589	21.6	0.4	59	12	AAH9165	Oligonucleotide OD	c 662	21.4	0.4	64	21	ABK31823	Human secreted pro
c 590	21.6	0.4	60	16	AAK094939	Single chain Fv ju	c 663	21.4	0.4	65	24	ABK32088	Human secreted pro
c 591	21.6	0.4	60	24	ABN36150	Human spliced tran	c 664	21.4	0.4	65	24	ABK53109	Mouse spliced tran
c 592	21.6	0.4	60	24	ABN36355	Human spliced tran	c 665	21.4	0.4	65	24	ABK57332	Mouse spliced tran
c 593	21.6	0.4	60	24	ABN42265	Human spliced tran	c 666	21.4	0.4	66	22	AAK14777	Hepatitis E virus

c 667	21.4	0.4	75	18	AAT73662	Promoter-primer HB
c 668	21.4	0.4	75	22	AA67947	HBV oligonucleotid
c 669	21.4	0.4	78	22	AA69817	Human foetal liver
c 670	21.4	0.4	78	22	AAK18013	Human brain expres
c 671	21.4	0.4	78	22	AAK43898	Human bone marrow
c 672	21.4	0.4	78	22	AA149908	Probe #18594 used
c 673	21.4	0.4	78	24	AB518128	Human genome-deriv
c 674	21.4	0.4	79	16	AAT00281	Full length bFGF f
c 675	21.4	0.4	79	22	ABA72993	Human foetal liver
c 676	21.4	0.4	79	22	AAK21425	Human brain expres
c 677	21.4	0.4	79	22	AAK47586	Human bone marrow
c 678	21.4	0.4	79	22	AA153418	Probe #22104 used
c 679	21.4	0.4	80	19	AA053251	bFGF family 1 ligat
c 680	21.4	0.4	80	19	AA053251	Probe to gene enco
c 681	21.4	0.4	80	19	AAV37925	Platelet derived e
c 682	21.4	0.4	80	22	ABA50886	Human breast cell
c 683	21.4	0.4	80	22	ABA68859	Human foetal liver
c 684	21.4	0.4	80	22	ABA35812	Probe #14278 for g
c 685	21.4	0.4	80	22	AAK17195	Human brain expres
c 686	21.4	0.4	80	22	AAK42977	Human bone marrow
c 687	21.4	0.4	80	22	AA123745	Probe #13678 for g
c 688	21.4	0.4	80	22	AA149057	Probe #17743 used
c 689	21.4	0.4	80	22	AA109356	Probe #9347 used t
c 690	21.4	0.4	80	24	AB517046	Human genome-deriv
c 691	21.4	0.4	82	19	AAV64898	HSV-1 latency asso
c 692	21.4	0.4	83	21	AAAC23155	Human secreted pro
c 693	21.4	0.4	83	21	AA119479	Human breast cance
c 694	21.4	0.4	84	21	AAK12602	Human secreted pro
c 695	21.4	0.4	85	19	AAV05667	Human cathepsin K
c 696	21.4	0.4	86	19	AAV25368	PCR primer used to
c 697	21.4	0.4	87	15	AA044722	Oligonucleotide us
c 698	21.4	0.4	87	20	AA28556	Oligonucleotide C2
c 699	21.4	0.4	89	22	AA676692	Insulator plasmid
c 700	21.4	0.4	90	22	AA116665	dAMP-specific apta
c 701	21.4	0.4	90	24	ABK36244	HIV DNA encoding G
c 702	21.4	0.4	90	24	ABK36558	HCY DNA encoding H
c 703	21.4	0.4	92	17	AA139467	Growth regulatory
c 704	21.4	0.4	92	19	AAV37485	Human growth regul
c 705	21.4	0.4	94	18	AA65372	Platelet derived g
c 706	21.4	0.4	94	20	AAV05728	Nucleotide sequenc
c 707	21.4	0.4	94	20	AAK87059	Platelet derived g
c 708	21.4	0.4	94	21	AAK36716	MuV and MV fusion
c 709	21.4	0.4	94	22	ABA71992	Human foetal liver
c 710	21.4	0.4	94	22	AAK04117	Human brain expres
c 711	21.4	0.4	94	22	AAK46558	Human bone marrow
c 712	21.4	0.4	94	22	AA152394	Probe #21080 used
c 713	21.4	0.4	94	22	AA507786	Cervical cancer pr
c 714	21.4	0.4	95	21	AAK19442	Human secreted pro
c 715	21.4	0.4	97	15	AA044725	Oligonucleotide us
c 716	21.4	0.4	97	19	AAV81329	Oligonucleotide HL
c 717	21.4	0.4	97	19	AAV81326	Oligonucleotide HL
c 718	21.4	0.4	97	19	AAV81327	Oligonucleotide HL
c 719	21.4	0.4	97	19	AAV68582	Nucleotide sequenc
c 720	21.4	0.4	97	20	AA28559	Oligonucleotide C2
c 721	21.4	0.4	97	22	AAH74754	Oligonucleotide us
c 722	21.4	0.4	97	22	AAH74755	Oligonucleotide us
c 723	21.4	0.4	97	22	AAH74757	Oligonucleotide HL
c 724	21.4	0.4	97	24	ABA95552	Oligonucleotide HL
c 725	21.4	0.4	97	24	ABA95553	Oligonucleotide HL
c 726	21.4	0.4	97	24	ABA95555	Oligonucleotide HL
c 727	21.4	0.4	98	12	AAQ11764	Self-complementary
c 728	21.4	0.4	98	21	AAA49117	1465-110 primer us
c 729	21.4	0.4	99	17	AAT30873	Primer 3 for 95 kD
c 730	21.4	0.4	99	21	AAAC98715	Human colon cancer
c 731	21.4	0.4	99	22	AAK32104	Human HFGAN72 rece
c 732	21.4	0.4	100	19	AAV64902	HSV-1 latency asso
c 733	21.4	0.4	100	20	AAK90537	Erythropoietin 3'-
c 734	21.4	0.4	100	20	AAK25700	Human erythropoiet
c 735	21.4	0.4	100	24	ABK95737	Plant expression c
c 736	21.4	0.4	100	24	ABK83304	Human ovarian can
c 737	21.2	0.4	30	21	AAZ55622	Human BMP-7 exon 1
c 738	21.2	0.4	41	22	AAH43320	Human zinc-finger
c 739	21.2	0.4	47	21	AAZ65938	Human map-related
c 740	21.2	0.4	47	22	AAZ75504	Prospero gene poly
c 741	21.2	0.4	48	20	AAK27676	Potato Lectin HRGP
c 742	21.2	0.4	48	24	ABK51786	Hydroxyproline-ric
c 743	21.2	0.4	50	22	AAK33859	Human SNP oligonuc
c 744	21.2	0.4	51	22	AAK30895	Human SNP oligonuc
c 745	21.2	0.4	51	22	AAK131710	Human SNP oligonuc
c 746	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 747	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 748	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 749	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 750	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 751	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 752	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 753	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 754	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 755	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 756	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 757	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 758	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 759	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 760	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 761	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 762	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 763	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 764	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 765	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 766	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 767	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 768	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 769	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 770	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 771	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 772	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 773	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 774	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 775	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 776	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 777	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 778	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 779	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 780	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 781	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 782	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 783	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 784	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 785	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 786	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 787	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 788	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 789	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 790	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 791	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 792	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 793	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 794	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 795	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 796	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 797	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 798	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 799	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 800	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 801	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 802	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 803	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 804	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 805	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 806	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 807	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 808	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 809	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 810	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 811	21.2	0.4	51	22	AAK32301	Human SNP oligonuc
c 812	21.2	0.4	51	22	AAK32301	Human SNP oligonuc

C 813	21.2	0.4	87	21	AA245772	PCR primer 1 used	886	21	0.4	60	24	ABN33910	Human spliced tran
C 814	21.2	0.4	87	22	AAH20156	Human breast cancer	887	21	0.4	60	24	ABN34975	Human spliced tran
C 815	21.2	0.4	87	22	AAH74733	Probe used identifi	888	21	0.4	60	24	ABN38126	Human spliced tran
C 816	21.2	0.4	87	24	AAD37584	Oligo #1 used in t	889	21	0.4	60	24	ABN39630	Human spliced tran
C 817	21.2	0.4	89	16	AAH23700	Human gene signatu	C 890	21	0.4	60	24	ABN41230	Human spliced tran
C 818	21.2	0.4	90	21	AAH29843	Human colon cancer	891	21	0.4	60	24	ABN41494	Human spliced tran
C 819	21.2	0.4	90	22	ABA50328	Human breast cell	892	21	0.4	60	24	ABN42411	Human spliced tran
C 820	21.2	0.4	90	22	ABA68274	Human foetal liver	893	21	0.4	60	24	ABN43599	Human spliced tran
C 821	21.2	0.4	90	22	ABA35281	Probe #13747 for g	894	21	0.4	60	24	ABN46545	Human spliced tran
C 822	21.2	0.4	90	22	AAH16649	Human brain expres	895	21	0.4	60	24	ABN46597	Human spliced tran
C 823	21.2	0.4	90	22	AAH24243	Human bone marrow	896	21	0.4	64	17	AAH73726	Human spliced tran
C 824	21.2	0.4	90	22	AAH23211	Probe #13104 for g	897	21	0.4	64	18	AAH12557	Human spliced tran
C 825	21.2	0.4	90	22	AAH48490	Probe #17176 used	898	21	0.4	65	24	ABN28776	Human spliced tran
C 826	21.2	0.4	90	22	AAH08826	Probe #8817 used t	C 899	21	0.4	65	24	ABN30802	Human spliced tran
C 827	21.2	0.4	90	24	ABH16466	Human genome-deriv	C 900	21	0.4	65	24	ABN31705	Human spliced tran
C 828	21.2	0.4	90	24	AAH172464	18 aa linker const	C 901	21	0.4	65	24	ABN52349	Human spliced tran
C 829	21.2	0.4	90	24	ABH36561	HCV DNA encoding H	C 902	21	0.4	65	24	ABN53437	Human spliced tran
C 830	21.2	0.4	90	24	ABH36582	HCV DNA encoding H	C 903	21	0.4	65	24	ABN54930	Human spliced tran
C 831	21.2	0.4	90	24	ABH36714	Human DNA encoding	C 904	21	0.4	69	16	AAH05342	Human spliced tran
C 832	21.2	0.4	90	24	ABH36776	Human DNA encoding	C 905	21	0.4	69	20	AAH50512	Human spliced tran
C 833	21.2	0.4	91	16	AAH25335	Human gene signatu	C 906	21	0.4	70	21	AAH64592	Human spliced tran
C 834	21.2	0.4	91	16	AAH25335	Human gene signatu	C 907	21	0.4	72	11	AAH05247	Human spliced tran
C 835	21.2	0.4	92	16	AAH25335	Human gene signatu	C 908	21	0.4	72	16	AAH05881	Human spliced tran
C 836	21.2	0.4	93	16	AAH25335	Human gene signatu	C 909	21	0.4	72	19	AAH37921	Human spliced tran
C 837	21.2	0.4	93	16	AAH25335	Human gene signatu	C 910	21	0.4	72	21	AAH36689	Human spliced tran
C 838	21.2	0.4	96	24	AAH46571	Oligonucleotide SE	C 911	21	0.4	74	18	AAH03803	Human spliced tran
C 839	21.2	0.4	97	22	ABH48198	Human PAPalpha spe	C 912	21	0.4	74	18	AAH86719	Human spliced tran
C 840	21.2	0.4	97	22	ABH48198	Human PAPalpha spe	C 913	21	0.4	74	21	AAH28223	Human spliced tran
C 841	21.2	0.4	97	22	ABH33156	Human foetal liver	C 914	21	0.4	74	21	AAH30732	Human spliced tran
C 842	21.2	0.4	97	22	ABH33156	Human foetal liver	C 915	21	0.4	74	22	AAH82937	Human spliced tran
C 843	21.2	0.4	97	22	AAH40242	Human brain expres	C 916	21	0.4	75	22	AAH13048	Human spliced tran
C 844	21.2	0.4	97	22	AAH21006	Human bone marrow	C 917	21	0.4	76	16	AAH09880	Human spliced tran
C 845	21.2	0.4	97	22	AAH46257	Probe #10939 for g	C 918	21	0.4	78	15	AAH068620	Human spliced tran
C 846	21.2	0.4	97	22	AAH46257	Probe #14943 used	C 919	21	0.4	78	15	AAH068620	Human spliced tran
C 847	21.2	0.4	97	22	AAH46257	Probe #6712 used t	C 920	21	0.4	78	15	AAH068622	Human spliced tran
C 848	21.2	0.4	98	21	AAH53447	Human genome-deriv	C 921	21	0.4	78	22	AAH22250	Human spliced tran
C 849	21.2	0.4	100	21	AAH72286	Human thiorodoxin	C 922	21	0.4	78	22	AAH20115	Human spliced tran
C 850	21.2	0.4	100	22	AAH20708	Human foetal liver	C 923	21	0.4	79	19	AAH32414	Human spliced tran
C 851	21.2	0.4	100	22	AAH20708	Human foetal liver	C 924	21	0.4	79	22	AAH32414	Human spliced tran
C 852	21.2	0.4	100	23	AAH46854	Human brain expres	C 925	21	0.4	79	22	AAH32414	Human spliced tran
C 853	21.2	0.4	100	23	AAH46854	Human brain expres	C 926	21	0.4	79	22	AAH32414	Human spliced tran
C 854	21.2	0.4	100	23	AAH46854	Human brain expres	C 927	21	0.4	79	22	AAH32414	Human spliced tran
C 855	21.2	0.4	100	23	AAH46854	Human brain expres	C 928	21	0.4	80	22	AAH32414	Human spliced tran
C 856	21.2	0.4	100	23	AAH46854	Human brain expres	C 929	21	0.4	80	22	AAH32414	Human spliced tran
C 857	21.2	0.4	100	23	AAH46854	Human brain expres	C 930	21	0.4	81	16	AAH06210	Human spliced tran
C 858	21.2	0.4	100	23	AAH46854	Human brain expres	C 931	21	0.4	81	16	AAH06210	Human spliced tran
C 859	21.2	0.4	100	23	AAH46854	Human brain expres	C 932	21	0.4	81	21	AAH76118	Human spliced tran
C 860	21.2	0.4	100	23	AAH46854	Human brain expres	C 933	21	0.4	82	20	AAH20708	Human spliced tran
C 861	21.2	0.4	100	23	AAH46854	Human brain expres	C 934	21	0.4	84	19	AAH50396	Human spliced tran
C 862	21.2	0.4	100	23	AAH46854	Human brain expres	C 935	21	0.4	84	19	AAH50396	Human spliced tran
C 863	21.2	0.4	100	23	AAH46854	Human brain expres	C 936	21	0.4	85	22	AAH72134	Human spliced tran
C 864	21.2	0.4	100	23	AAH46854	Human brain expres	C 937	21	0.4	85	22	AAH72134	Human spliced tran
C 865	21.2	0.4	100	23	AAH46854	Human brain expres	C 938	21	0.4	85	22	AAH72134	Human spliced tran
C 866	21.2	0.4	100	23	AAH46854	Human brain expres	C 939	21	0.4	85	22	AAH72134	Human spliced tran
C 867	21.2	0.4	100	23	AAH46854	Human brain expres	C 940	21	0.4	85	22	AAH72134	Human spliced tran
C 868	21.2	0.4	100	23	AAH46854	Human brain expres	C 941	21	0.4	85	22	AAH72134	Human spliced tran
C 869	21.2	0.4	100	23	AAH46854	Human brain expres	C 942	21	0.4	86	20	AAH85126	Human spliced tran
C 870	21.2	0.4	100	23	AAH46854	Human brain expres	C 943	21	0.4	86	22	AAH85126	Human spliced tran
C 871	21.2	0.4	100	23	AAH46854	Human brain expres	C 944	21	0.4	86	22	AAH85126	Human spliced tran
C 872	21.2	0.4	100	23	AAH46854	Human brain expres	C 945	21	0.4	86	22	AAH85126	Human spliced tran
C 873	21.2	0.4	100	23	AAH46854	Human brain expres	C 946	21	0.4	88	14	AAH044254	Human spliced tran
C 874	21.2	0.4	100	23	AAH46854	Human brain expres	C 947	21	0.4	88	14	AAH044254	Human spliced tran
C 875	21.2	0.4	100	23	AAH46854	Human brain expres	C 948	21	0.4	90	19	AAH42312	Human spliced tran
C 876	21.2	0.4	100	23	AAH46854	Human brain expres	C 949	21	0.4	90	24	AAH94640	Human spliced tran
C 877	21.2	0.4	100	23	AAH46854	Human brain expres	C 950	21	0.4	90	24	AAH94640	Human spliced tran
C 878	21.2	0.4	100	23	AAH46854	Human brain expres	C 951	21	0.4	91	22	AAH94640	Human spliced tran
C 879	21.2	0.4	100	23	AAH46854	Human brain expres	C 952	21	0.4	91	22	AAH94640	Human spliced tran
C 880	21.2	0.4	100	23	AAH46854	Human brain expres	C 953	21	0.4	91	22	AAH94640	Human spliced tran
C 881	21.2	0.4	100	23	AAH46854	Human brain expres	C 954	21	0.4	91	22	AAH94640	Human spliced tran
C 882	21.2	0.4	100	23	AAH46854	Human brain expres	C 955	21	0.4	91	22	AAH94640	Human spliced tran
C 883	21.2	0.4	100	23	AAH46854	Human brain expres	C 956	21	0.4	91	22	AAH94640	Human spliced tran
C 884	21.2	0.4	100	23	AAH46854	Human brain expres	C 957	21	0.4	91	22	AAH94640	Human spliced tran
C 885	21.2	0.4	100	23	AAH46854	Human brain expres	C 958	21	0.4	91	22	AAH94640	Human spliced tran

959 21 0.4 91 22 AAI08407 used t
 960 21 0.4 91 24 ABS15999 Human genome-deriv
 961 21 0.4 91 24 ABS23428 Human genome-deriv
 962 21 0.4 92 17 AAT28981 Antisense internal
 963 21 0.4 92 22 AAT28981 Ganglioside GD3 sp
 964 21 0.4 93 16 AAT18954 oligonucleotide p2
 965 21 0.4 93 16 AAO99844 Haematopoietic mat
 966 21 0.4 93 16 AAO90523 oxalyl-CoA decarbo
 967 21 0.4 93 17 AAT37260 VDJ joint sequence
 968 21 0.4 93 18 AAT12555 VH251 DHQ52 J6 mu
 969 21 0.4 93 18 AAT7518 5' primer for cDNA
 970 21 0.4 93 24 AAZ37460 PCR primer for hum
 971 21 0.4 93 24 AAD27922 Human haemopoietic
 972 21 0.4 94 17 AAT37271 VDJ joint sequence
 973 21 0.4 94 18 AAV12566 VH105 D2 J6 mu c10
 974 21 0.4 94 21 AAC09026 Human secreted pro
 975 21 0.4 94 22 AAK24216 Human brain expres
 976 21 0.4 94 22 AAK56209 Probe #24895 used
 977 21 0.4 96 20 AAV81029 De-immunised 340 V
 978 21 0.4 97 22 AAC14667 Human secreted pro
 979 21 0.4 97 22 ABA47501 Human breast cell
 980 21 0.4 97 22 ABA65391 Human foetal liver
 981 21 0.4 97 22 ABA32489 Probe #10955 for g
 982 21 0.4 97 22 AAK13800 Human brain expres
 983 21 0.4 97 22 AAK39545 Human bone marrow
 984 21 0.4 97 22 AAI20353 Probe #10286 for g
 985 21 0.4 97 22 AAI45558 Probe #14244 used t
 986 21 0.4 97 22 AAI06055 Probe #6046 used t
 987 21 0.4 97 23 AAS58791 cDNA #1467 encodin
 988 21 0.4 97 24 ABS13634 Human genome-deriv
 989 21 0.4 98 19 AAV73256 C. utilis crtI p1
 990 21 0.4 98 22 ABA49048 Human breast cell
 991 21 0.4 98 22 AAK1132 Human bone marrow
 992 21 0.4 98 22 AAI21894 Probe #11827 for g
 993 21 0.4 98 22 AAI47179 Probe #15865 used t
 994 21 0.4 98 22 AAI07583 Probe #7574 used t
 995 21 0.4 99 17 AAT37255 VDJ joint sequence
 996 21 0.4 99 18 AAV12550 VH251 DHQ52 J6 mu
 997 21 0.4 99 22 AAH36796 Human colon cancer
 998 21 0.4 99 24 ABL82637 Human ovarian canc
 999 21 0.4 100 26 AAT22067 Human gene signatu
 1000 20.8 47 21 AAZ68084 Human map-related

ALIGNMENTS

RESULT 1
 ABN34264
 ID ABN34264 standard; DNA; 60 BP.

AC ABN34264;
 DT 15-JUL-2002 (first entry)
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:7012.
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:7012.
 DE Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 OS Homo sapiens.
 OS WO200210449-A2.

PD 07-FEB-2002.
 PF 20-JUL-2001; 2001WO-IB01903.
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 DR WPI; 2002-257383/30.
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting "tissue", "pathology", and
 PT developmental-specific genes
 XX Example 1; SEQ ID 7012; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcript unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition, to detect developmental specific genes, and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN77253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 60 BP; 17 A; 16 C; 14 G; 13 T; 0 other;
 Query Match 1.2%; Score 60; DB 24; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4479 AACTCTGAGTTACTTCCCGAGTGCTAATCAGTGACAGCAGTGACAGCTCGA 4538
 DB 1 AACTCTGAGTTACTTCCCGAGTGCTAATCAGTGACAGCAGTGACAGCTCGA 60

RESULT 2
 ABN52341
 ID ABN52341 standard; DNA; 65 BP.

AC ABN52341;
 DT 15-JUL-2002 (first entry)
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25089.
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25089.
 DE Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 OS Mus musculus.

PD 07-FEB-2002.
 PF 20-JUL-2001; 2001WO-IB01903.
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX WP1: 2002-257383/30.
 DR
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1: SEQ ID 25089; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN9589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 65 BP; 15 A; 14 C; 18 G; 18 T; 0 other;
 XX
 Query Match 1.1%; Score 55.4; DB 24; Length 65;
 Best Local Similarity 90.8%; Pred. No. 0.0066;
 Matches 59; Conservative 0; Mismatches 6; Indels 0; Gaps 0
 OY 4742 AGTCTTGCTACCTCCCTACGGAAGAAACAAATTCCTTGCACTTATGCAATGCGT 4801
 Db 1 AAGTTCTTGCTACCTCCCTGCAAGAAACAAAGTCTTGCACTTATGCAAGTGGCG 60
 OY 4802 TTAGG 4806
 Db 61 GTAGG 65
 RESULT 3
 AAI30935
 ID AAI30935 standard; DNA; 31 BP.
 AC AAI30935;
 XX
 DT 18-OCT-2001 (first entry)
 DE Human-single nucleotide polymorphism (SNP) GLI3 1.
 XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KM single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(16,C)
 FT /*tag= a
 XX /standard_name= "single nucleotide polymorphism"
 PN WO200166800-A2.
 XX

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PD    13-SEP-2001.
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PF      07-MAR-2001; 2001WO-US07268.
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XX
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PR      07-MAR-2000; 200OUS-0187510.
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PR     22-MAY-2000; 200OUS-0206129.
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XX
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PA      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
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XX
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Cargill M, Ireland JS, Lander ES;
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DR     WPI; 2001-522952/57.
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XX
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```
PT Nucleic acid molecules from the human genome which include polymorphic
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PT sites, useful in methods for predicting the presence, absence or
```

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PT severity of a particular phenotype or disorder (e.g. diabetes)
```

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PT associated with a particular genotype -
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XX
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PS Claim I, Page 117; 145pp; English.
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The invention relates to the identification of nucleic acid molecules
which can predispose individuals to disease. Various genes from a number
of individuals were resequenced and single nucleotide polymorphisms
(SNPs) in these genes discovered. The method is useful for predicting the
presence, absence or severity of a particular phenotype or disorder (e.g.
diabetes) associated with a particular genotype. The nucleic acids
containing the polymorphic sites may be useful in forensics and paternity
testing.

```
SQ Sequence 31 BP; 5 A; 15 C; 10 G; 1 T; 0 other;
```

```
Oy Query Match           0.6%; Score 31; DB 20; Length 31;  
Best Local Similarity   100.0%; Pred.No.1.seg=3;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

```
Dy 2865 AGGAGGCCCGCCGGCAGACGCCTGTCCCAC 2895  
Db 1 AGGAGGCCCGCCGGCAGACGCCTGTCCCAC 31  
|||||  
|||
```

```
RESULT 4  
AI30936  
ID AI30936 standard; DNA; 31 BP.  
XX  
AC  
AAI30936;  
XX  
DT 18-OCT-2001 (first entry)  
DE Human single nucleotide polymorphism (SNP) GLI3 2.  
XX  
KW Human; resequencing; genotyping; disease; forensic; paternity testing;  
single nucleotide polymorphism; SNP; ss.  
XX  
OS Homo sapiens.  
CS Key Location/Qualifiers  
FH Variation replace(16,C)  
FT /tag=a  
FT /standard_name="single nucleotide polymorphism"  
PN WO200166800-A2.  
PD 13-SEP-2001.  
XX  
PF 07-MAR-2001; 2001WO-US07268.  
XX  
PR 07-MAR-2000; 200OUS-0187510.  
PR 22-MAY-2000; 200OUS-0206129.  
XX  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
Cargill M, Ireland JS, Lander ES;  
PI
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XX Sequence 88 BP; 30 A; 24 C; 32 G; 2 T; 0 other;
 SQ
 Query Match 0.6%; Score 28; DB 22; Length 88;
 Best Local Similarity 60.5%; Pred. No. 1.1e+04;
 Matches 46; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 2565 CGTCACTAGCTGTAACATGCTCAACAGAGGAGCAGCGCCGACCATCATGCTCGGC 2624
 DB 3 CGTCACTAGCTGTAACATGCTCAACAGAGGAGCAGCGCCGACCATCATGCTCGGC 62

OY 2625 CTACCTGAGAGCGCCG 2640
 DB 63 CAGCAGGAGCAGCAGC 78

RESULT 10
 AAS13081
 ID AAS13081 standard; DNA; 75 BP.
 AC AAS13081;
 DT 17-DEC-2001 (first entry)
 DE DNA encoding zinc finger domain TG-ZFD-040.
 XX
 KW Zinc finger domain; cancer; human; ds.
 OS Homo sapiens.
 PN WO200160970-A2.
 PD 23-AUG-2001.
 PF 17-FEB-2001; 2001WO-KR00244.
 XX
 PR 18-FEB-2000; 2000KR-0007730.
 PA (TOOL-) TOOLGEN INC.
 PI Kim J, Kwon Y, Kim H, Ryu EH, Hwang MS;
 DR WPI: 2001-557644/62.
 P-PSDB; AAU08533.

PT Identifying a zinc finger domain for e.g. designing new polypeptides
 PT that bind to a specific site on a DNA, comprises expressing hybrid
 PT nucleic acids with a test zinc finger domain in cells -
 XX
 PS Example 49; Page 66; 147bp; English.

XX The invention relates to a method of identifying a zinc finger domain
 CC that recognises a target site on a DNA. The method comprises expressing
 CC hybrid nucleic acids with a test zinc finger domain in cells containing a
 CC reporter construct, where the reporter gene is expressed above a given
 CC level when a transcription factor recognises a recruitment and a target
 CC site of a promoter, and not only the recruitment site of the promoter.
 CC The method is used to: (a) identify a zinc finger domain that recognises
 CC a target site on a DNA; (b) determine whether a test zinc finger domain
 CC recognises a target site on a promoter; (c) generate a nucleic acid that
 CC encodes a chimeric zinc finger protein; and (d) identify DNA sequences
 CC recognised by zinc finger domains. The method can be used to design novel
 CC polypeptides that bind to a specific site on a DNA. The method can
 CC facilitate the customised generation of new polypeptides that can
 CC regulate the expression of a selected target e.g. a gene required by a
 CC pathogen can be repressed, a gene required for cancerous growth can be
 CC repressed, or a gene poorly expressed or encoding a mutated protein can
 CC be activated and overexpressed. The method can be used in vivo which
 CC enables identification of polypeptides that bind to a specific site on a
 CC DNA in the intracellular milieu. The present sequence represents the
 CC coding sequence of TG-ZFD-040 zinc finger protein which was used in
 CC the method of the invention.

SQ Sequence 75 BP; 17 A; 25 C; 22 G; 11 T; 0 other;
 Query Match 0.5%; Score 27.6; DB 22; Length 75;
 Best Local Similarity 67.2%; Pred. No. 1.2e+04;
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1496 ACTGCCACTGGGAGGCTGCGGAGGAGTTCGACCCAGAGAGCTTGACCA 1553
 DB 5 ACTGCCACTGGGAGGCTGCGGAGGAGTTCGACCCAGAGAGCTTGACCA 62

RESULT 11
 ABK36865
 ID ABK36865 standard; DNA; 90 BP.
 AC ABK36865;
 DT 08-MAY-2002 (first entry)
 DE Human DNA encoding MAGE-3 segment 2.
 XX
 KW Sayine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia; ds.
 OS Homo sapiens.
 PN WO200190197-A1.
 PD 29-NOV-2001.
 PF 25-MAY-2001; 2001WO-AU00622.
 XX
 PR 26-MAY-2000; 2000AU-0007761.
 PA (AUSU) UNIV AUSTRALIAN NAT.
 PI Thomson SA, Ramshaw JA;
 DR WPI: 2002-147575/19.
 P-PSDB; AAU85045.

PT New synthetic polypeptides having several different segments of at
 PT least one parent polypeptide linked together differently compared to
 PT the linkage in the parent polypeptide, for inducing immune response
 PT against a pathogen or cancer -
 XX
 PS Example 3; Fig 27; 364bp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for
 CC designing the synthetic polypeptides. The synthetic polypeptides and
 CC polynucleotides are referred to as a vaccine. The synthetic polypeptide is
 CC useful for modulating immune responses preferably directed against a
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
 CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present
 CC sequence encodes a peptide derived from a parent protein used to
 CC construct a vaccine of the invention.

Query Match	Similarity	Score	DB	Length
Best Local	45%	60.8	Pred. No. 1.3e+04	95
Matches	45	Conservative	0	Mismatches 29; Indels 0; Gaps 0
Db	3227	GAAGTTCACATCGTCCCTCTCCTCCAGCATCAGCAGAAAGCTGAGATGCC	3286	
QY	82	GAAGTTCACATCGTCCCTCTCCTCCAGCATCAGCAGAAAGCTGAGATGCC	23	
Db	3287	TGACCATGACGCT	3300	
QY	22	TGGGAACGACGCT	9	
RESULT 13				
AT27118				
ID	AT27118	standard; DNA; 99	BP.	
AC	AT27118;			
XX	06-AUG-1996	(first entry)		
DT	Hepatitis E virus (Mexico strain)	406.4-2 antigen DNA.		
XX	Hepatitis E virus (Mexico strain)	406.4-2 antigen DNA.		
DE	HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;			
XX	diagnosis; antigen; ds.			
KW	Hepatitis E virus Mexico strain.			
XX	WO9612807-A2.			
XX	02-MAY-1996.			
XX	23-OCT-1995;	95WO-US13703.		
XX	13-OCT-1995;	95US-0542634.		
XX	24-OCT-1994;	94US-0327952.		
XX	(GENE-) GENELABS TECHNOLOGIES INC.			
PA	Fuerst TR, McAttee CP, Yarbrough PO, Zhang Y;			
PI	WPI: 1996-230608/23.			
XX	P-PSDB: AAR96100.			
DR	Disclosure: Page 78; 125pp; English.			
XX	A DNA sequence (AA77118) codes for a C-terminal fragment (AAR96100),			
CC	406.4-2, of a structural protein (see also AAR96098) of hepatitis			
CC	E virus (HEV) Mexico strain. It can be obtd. from phage lambda			
CC	gt11 clone 406.3-2, which includes the HEV Mexico ORF-2 (AA72108)			
CC	and ORF-3 (AA72116). The DNA is inserted into pCEV for expression			
CC	of 406.4-2 antigen in E. coli. The antigen can be utilised in			
CC	diagnostic assays of HEV when used in conjunction with 62K antigens			
CC	(see also AAR96091-92 and AAR96101-04) of HEV capsid protein.			
XX	Sequence 99 BP; 12 A; 46 C; 29 G; 12 T; 0 other;			
SQ	Query Match	0.5%	Score 27.6;	DB 21; Length 95;
XX	Best Local Similarity	55.9%	Pred. No. 1.5e+04;	
XX	Matches	52;	Conservative	0; Mismatches 41; Indels 0; Gaps 0;

Matches	34;	Conservative	0;	Mismatches	12;	Indels	0;	Gaps
Qy	4661	TTTGCTTTGGCGCTTTT	TAGTTCGATGATGATTTT	AGCATCTC	4906			
Db	1	TTTTTTTTTTTTTTTTTTTT	TTTGGCATGCTTTT	AACATCCC	46			
RESULT 16								
ID	AAI28394	standard; DNA; 51 BP.						
XX	AAI28394:							
DT	24-JAN-2002	(first entry)						
DE	Human	SNP oligonucleotide #1602.						
XX								
KW	Immunosuppressive;	immunostimulatory; antiinflammatory; cytostratic;						
KW	neuroprotective;	antimicrobial; gene therapy; vaccine; amylase; cancer;						
KW	amyloid protein;	angiotensin; apoptosis related protein; cathepsin;						
KW	cyclin;	polymerase; oncogene; histone; kinase; colony stimulating factor;						
KW	complement related protein;	cytochrome; kinesin; cytokine; interferon;						
KW	interleukin; G-protein coupled receptor;	thioesterase; inflammation;						
KW	multifactorial disease;	autoimmune disease; infection;						
KW	nervous system disease;	ss.						
OS	Homo sapiens.							
PN	W0200147944-A2.							
XX								
PD	05-JUL-2001.							
XX								
PF	28-DEC-2000;	2000MO-US35498.						
XX								
PR	28-DEC-1999;	99US-0173419.						
XX								
PR	27-DEC-2000;	2000US-0173419.						
XX								
PA	(CURA-) CURAGEN CORP.							
PI	Shinkets RA, Leach M;							
XX								
DR	WPI; 2001-465210/50.							
XX								
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,							
PT	oncogenes and histones, useful for diagnosing and treating, e.g.							
PT	cancer, autoimmune diseases and infections -							
XX								
PS	Claim 1; Page 1839; 4143pp; English.							
XX								
CC	The present invention relates to oligonucleotides encoding polymorphic							
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,							
CC	apoptosis related proteins, cathepsin, cyclin, polymerase, oncogenes,							
CC	histones, kinases, colony stimulating factors, complement related							
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins,							
CC	G-protein coupled receptors and thioesterases. The present sequence is							
CC	one such oligonucleotide. The oligonucleotides and the peptides encoded							
CC	by them may be used in the prevention, diagnosis and treatment of							
CC	diseases associated with inappropriate expression of the proteins listed							
CC	above. Disorders that may be prevented, diagnosed and/or treated include							
CC	multifactorial diseases with a genetic component, such as autoimmune							
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,							
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer							
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,							
CC	leukemia), diseases of the nervous system and an infection of pathogenic							
CC	organisms.							
XX								
XX	Sequence 51 BP; 6 A; 9 C; 3 G; 33 T; 0 other;							
Query Match	0.5%;	Score 26.8;	DB 22;	Length 51;				
Best Local Similarity	73.9%;	Pred. No. 1.6e+04;						
Matches 34;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0				
4661	TTTGCTTTGGCGCTTTT	TAGTTCGATGATGATTTT	AGCATCTC	4906				

Db	1	TTTTTTTTTTTTTTTTTTTTTTTTTGCATGCTGTTTAAACAATCCC	46
RESULT 17			
AAV17230			
AAV17230 standard; DNA; 75 BP.			
AC	AAV17230;		
XX			
XX	29-JUN-1998 (first entry)		
DT			
XX	SCA2 gene CAG repeat unit fragment.		
DE			
XX	SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.		
KW	Synthetic.		
XX			
OS	WO9803679-A1.		
XX			
PN	29-JAN-1998.		
XX			
PD	18-JUL-1996; 96WO-JP01999.		
XX			
PF	18-JUL-1996; 96WO-JP01999.		
XX			
PR	18-JUL-1996; 96WO-JP01999.		
XX			
PA	(SRLS-) SRL INC.		
XX			
PI	Sanpei K, Tsuji S;		
XX			
XX	WPI: 1998-120796/11.		
DR			
XX			
PT	Diagnosing spinocerebellar ataxis type II - by PCR and determining		
PT	number of CAG repeat units		
XX			
PS	Disclosure; Page 13; 23pp; Japanese.		
XX			
CC	This sequence represents a fragment of the SCA2 gene. It can be used in		
CC	the method of the invention for diagnosing spinocerebellar ataxis type		
CC	II, by performing PCR on the test DNA using two primers hybridising to		
CC	parts of the SCA2 gene sequence, and determining the number of CAG		
CC	repeats in the amplified products. The method provides an easy means for		
CC	the diagnosis of spinocerebellar ataxis type II.		
XX			
XX			
SQ	Sequence 75 BP; 23 A; 29 C; 23 G; 0 U; 0 other;		
Query Match	0.5%; Score 26.4; DB 19; Length 75;		
Best Local Similarity	65.0%; Pred. No. 2.3e+04;		
Matches 39; Conservative	0; Mismatches 21; Indels 0; Gaps 0;		
QY	2586 CAACGAGAGGGGACGACGACGCGCCAGCCATCAGTCGGGCTTACCTGAGCAGCGCGCGTC	2645	
Db	13 CAGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGCGCGCC	72	
RESULT 18			
AAV17230			
AAV17230 standard; DNA; 51 BP.			
AC	AAV17230;		
XX			
XX	24-JAN-2002 (first entry)		
DT			
XX			
DE	Human SNP oligonucleotide #127.		
XX			
KW	Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;		
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;		
KW	amyloid protein; angiotensin; apoptosis related protein; cadherin;		
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;		
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;		
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;		
KW	multifactorial disease; autoimmune disease; infection;		
KW	nervous system disease; ss.		

XX OS Homo sapiens.
 XX PN W0200147944-A2.
 XX PD 05-JUL-2001.
 XX PF 28-DEC-2000; 2000MO-US35498.
 XX PR 28-DEC-1999; 99US-0173419.
 XX PR 27-DEC-2000; 2000US-0173419.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX cancer, autoimmune diseases and infections -
 XX PS Claim 1; Page 1434; 4143pp; English.
 XX CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX SQ Sequence 51 BP; 19 A; 11 C; 10 G; 11 T; 0 other;
 XX
 XX Query Match 0.5%; Score 26.2; DB 22; Length 51;
 XX Best Local Similarity 72.3%; Pred. No. 2.2e+04;
 XX Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 XX
 XX QY 1737 AAACCTGAAACACACTTGAGATCTCACACTGAGAGAAACCATACG 1783
 XX 2 AAACCTGATTGTACATCAGAGAACTCATACAGAGAGAAACCTATG 48
 XX DB
 XX RESULT 19
 XX AAV68382/C
 XX ID AAV68382 standard; DNA; 89 BP.
 XX AC AAV68382;
 XX XX
 XX DT 10-MAR-1999 (first entry)
 XX DE Clone #8 fragment identified by CAG repeat analysis method.
 XX XX
 XX CAG repeat; human; genome analysis; medical diagnostic;
 XX nucleic acid analysis; variation assessment; neurological disease;
 XX Huntington's chorea; PCR suppression; SS.
 XX OS Homo sapiens.
 XX XX
 XX PN W09849345-A1.
 XX PD 05-NOV-1998.
 XX PF 29-APR-1998; 98WO-US08616.

XX XX
 XX PR 29-APR-1997; 97US-0045078.
 XX XX
 XX PA (UYBO-) UNITIV BOSTON.
 XX XX
 XX PI Smith CL;
 XX DR WPI; 1998-594983/50.
 XX XX
 XX PT Analysing nucleic acid samples - using amplification primers which
 XX contain CAG or CTG tri-nucleotide repeats for differential display
 XX of samples from different sources
 XX PS Example; Page 32; 44pp; English.
 XX CC This sequence represents a fragment of a human CAG repeat containing
 CC clone DNA sequence isolated using the method of the invention. The method
 CC is for analysing nucleic acids in a sample, and comprises: (a) providing
 CC a sample containing nucleic acid, a first oligonucleotide primer
 CC comprising a CTG repeat, a second oligonucleotide primer comprising a
 CC CAG repeat and a polymerase and PCR reagents; (b) preparing the nucleic
 CC acid so that it is amplifiable; (c) amplifying the nucleic acid with the
 CC first and second primers; and (d) detecting the amplified product. The
 CC method is used to distinguish between the expression of genes in two or
 CC more biological samples, e.g. body fluids, cells, solid tissue or solid
 CC and liquid foods. It can be used in medical diagnostics, e.g. to
 CC differentiate between normal and diseased tissue or to assess the
 CC variation within monozygotic twin pairs. The method allows the isolation
 CC and analysis of genome subsets containing CAG repeats which are known to
 CC be important in a number of neurological diseases including Huntington's
 CC chorea. The method uses PCR suppression, in which only fragments which
 CC contain a target repeat are efficiently amplified. This allows accurate
 CC identification of differentially expressed genes in various cell types.
 CC Genome complexity is reduced by the new method which targets genomic
 CC subsets containing CAG repeats.
 XX SQ Sequence 89 BP; 2 A; 23 C; 37 G; 27 T; 0 other;
 XX
 XX Query Match 0.5%; Score 26.2; DB 19; Length 89;
 XX Best Local Similarity 56.3%; Pred. No. 2.7e+04;
 XX Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 XX
 XX QY 2598 CAGCAGCGCCAGACCATCAGCTCGGCTTACCTGAGCAGCCGCTTCAGGATCTC 2657
 XX DB 89 CAGCAGCAGCAGCAGCAGCAGCCACACAGCAGCAGCAGCAGCAGCAGCAG 30
 XX QY 2658 GCCCTGCTTCTCCACCCGCCGCTCCAG 2684
 XX DB 29 CAGCCCGACAGCAGCAGCAGCAGCAG 3
 XX
 XX RESULT 20
 XX AAX53913
 XX ID AAX53913 standard; DNA; 90 BP.
 XX AC AAX53913;
 XX XX
 XX DT 05-JUL-1999 (first entry)
 XX DE Human tryptase-I antisense oligonucleotide fragment.
 XX XX
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 XX impaired respiration; inflammation; lung disease;
 XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
 XX acute asthma; allergy; asthma; impeded respiration;
 XX respiratory distress syndrome; pain; cystic fibrosis;
 XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
 XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 XX prostate cancer; ss.
 XX OS Synthetic.

XX MO9913886-A1.
 XX
 XX 25-MAR-1999.
 XX
 XX 17-SEP-1998; 98WO-US19419.
 XX
 XX 09-JUN-1998; 98US-0093972.
 XX 17-SEP-1997; 97US-0059160.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 XX NYce JW;
 XX
 XX WPI; 1999-229400/19.
 XX
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 PS
 XX Disclosure; Page 45; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AAK52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAK5272-74. These multiple target
 CC oligonucleotides (specifically AAK5180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases, as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 XX
 XX Sequence 90 BP; 0 A; 31 C; 35 G; 9 T; 15 other;
 SQ
 Query Match 0.5%; Score 26.2; DB 20; Length 90;
 Best Local Similarity 51.8%; Pred. No. 2.7e+04;
 Matches 43; Conservative 9; Mismatches 31; Indels 0; Gaps 0;
 QY 2977 GCCCCAGAGAGTGCAGCGAGCGGGGAGCCGCTACGGGGCGGCCACCTGCAGCG 3036
 DB 5 GBCGTGGGCBGGGGCGCGCTGCGCCBGGGGCGCGCCBGCBCBGCBG 64
 QY 3037 CACGATGCGTGGGCGCACGGCGT 3059
 DB 65 GCTCBGCBTCTGCGCCBGGGBT 87

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200062736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US08020.
 XX
 XX 06-APR-1999; 99US-0127958.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 XX
 XX NYce JW;
 XX
 XX WPI; 2000-679539/66.
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 141; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 XX Sequence 90 BP; 0 A; 31 C; 35 G; 9 T; 15 other;
 SQ
 Query Match 0.5%; Score 26.2; DB 21; Length 90;
 Best Local Similarity 51.8%; Pred. No. 2.7e+04;
 Matches 43; Conservative 9; Mismatches 31; Indels 0; Gaps 0;
 QY 2977 GCCCCAGAGAGTGCAGCGAGCGGGGAGCCGCTACGGGGCGGCCACCTGCAGCG 3036
 DB 5 GBCGTGGGCBGGGGCGCGCTGCGCCBGGGGCGCGCCBGCBCBGCBG 64
 QY 3037 CACGATGCGTGGGCGCACGGCGT 3059
 DB 65 GCTCBGCBTCTGCGCCBGGGBT 87

RESULT 22

AAA33356 standard; DNA; 90 BP.

AAA33356;

28-JUL-2000 (first entry)

Low adenosine antisense oligonucleotide SEQ ID NO:1045.

Human: adenosine receptor; low adenosine antisense oligonucleotide; phosphotriester; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; anti-inflammatory; antiallergic; antihistaminic; cytosolic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

MO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNITV EAST CAROLINA.

Nyce JW;

WPI: 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -

Claim 18; Page 396; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have anti-inflammatory, antiallergic, antihistaminic, cytosolic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 90 BP; 0 A; 31 C; 35 G; 9 T; 15 other;

Query Match 0.5%; Score 26.2; DB 21; Length 90;

Best Local Similarity 51.8%; Pred. No. 2.7e+04; Matches 43; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 2977 GCCCGAGAGGTGACGAGGAGGAGCCACGAGTACGGGCGGACACTGCACCG 3036

DB 5 GBCGTGGGCGBGGGCGCGCTGCGCCBGBGCGGCGCGCGCGCGCGCG 64

QY 3037 CACGATGCGCTGGGCGGCGCGGT 3059

DB 65 GCTGCGCTCGTGGCGCGGCGGT 87

RESULT 23

AAT78908 standard; cDNA; 66 BP.

AAT78908;

09-FEB-1998 (first entry)

Poly-glutamine repeat region coding sequence from clone DAN1.

Monoclonal antibody; neurodegenerative disease; polyglutamine; TBP; repeat region; affinity; RNA binding protein; Kennedy disease; Huntington's disease; dominant autosomal spinocerebellar ataxia; X-linked spino-bulbar muscular atrophy; familial spastic paraplegia; dentatorubral-pallidolusial atrophy; bipolar affective disorder; manic depressive psychosis; ss.

Homo sapiens.

MO9717445-A1.

15-MAY-1997.

08-NOV-1996; 96WO-FR01773.

10-NOV-1995; 95FR-0013576.

(CNRS) CNRS CENT NAT RECH SCI.

(INRM) INSEPM INST NAT SANTE & RECH MEDICALE.

Lutz Y, Mandel J, Trollet Y;

WPI: 1997-281034/25.

Antibody 1C2 used for treating or preventing neuro-degenerative diseases - associated with proteins containing long poly:glutamine repeats, e.g. Huntington's disease

Claim 21; Page 43; 69pp; French.

The invention relates to a monoclonal antibody (MAB) 1C2 for the treatment of neurodegenerative diseases associated with the presence of polyglutamine repeat regions. This MAB is already known for its affinity to the RNA binding protein (TBP) transcription initiation factor, especially at the amino acid sequence LERQORQOQOQ found at the N-terminus of TBP. MAB 1C2 has been shown to have a high affinity for polyglutamine repeats with a proportional affinity to the number of glutamine repeats. This affinity has been used to identify genes encoding proteins containing long polyglutamine repeats which are implicated in neurodegenerative diseases. A screen of an expression library, generated from a lymphoblastic cell line from a patient suffering from spinocerebellar ataxia (SCA), with MAB 1C2 isolated 6 new sequences (AAT78906-778911) encoding polyglutamine repeats. This sequence is derived from clone DAN1 isolated from a patient suffering from dominant autosomal SCA type 7. MAB 1C2, active fragment of it or nucleic acids encoding it are specifically used to treat Huntington's disease, SCA types 1-5 or 7, X-linked spino-bulbar muscular atrophy (Kennedy disease), dentatorubral-pallidolusial atrophy, dominant autosomal spinocerebellar ataxia, familial spastic paraplegia, bipolar affective disorder, manic depressive psychoses and schizophrenia.

Sequence 66 BP; 24 A; 22 C; 20 G; 0 U; 0 other;

Matches 44; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

AC ABN52286;

```

XX 15-JUL-2002 (first entry)
XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:25034.
XX
DE Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN MO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1901903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes.
XX
PS Example 1; SEQ ID 25034; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition: to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN29589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 65 BP; 22 A; 13 C; 16 G; 14 T; 0 other;

```

Query Match 0.5%; Score 25.8; DB 24; Length 65;
 Best Local Similarity 63.9%; Pred. No. 3e+04; Mismatches 22; Indels 0; Gaps 0;
 Matches 39; Conservative 0;

```

QY 1626 GAAACCTTCAAGCCATATATGTGTAGTCATATGAGACACAGCGGAGGAGAA 1685
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 5 GAAACCTTATCAACCTCAGCTTACAGACATATGAGAAATCATACGAGAGAGAA 64
QY 1686 G 1686
DB 65 G 65

```

RESULT 27

```

AAD24301
ID AAD24301 standard; DNA; 74 BP.
XX
AC AAD24301;
XX
DT 07-MAR-2002 (first entry)
XX
DE der 22 DNA related to the invention.
XX
OS Genetic deletion; translocation; mutation; conotruncal defect;
XX DiGeorge syndrome; DGS; CHARGE association; Velocardiofacial syndrome;
XX Shprintzen syndrome; cleft palate; der 22; ds.
XX
OS Unidentified.
XX
PN US6303294-B1.
XX
PD 16-OCT-2001.
XX
PF 07-JUN-1995; 95US-0473319.
XX
PR 10-JUL-1992; 92US-0911534.
XX
PR 04-OCT-1991; 91US-0770758.
XX
PR 22-NOV-1993; 93US-0156672.
XX
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX (UYPE-) UNIV PENNSYLVANIA.
XX
PI Emanuel BS, Budarf ML, Driscoll D;
XX
DR WPI; 2002-033211/04.
XX
PT Novel methods to detect genetic changes associated with DiGeorge
XX syndrome, Velocardiofacial syndrome, CHARGE association, conotruncal
XX defect and/or cleft palate are useful for prenatal screening for the
XX diseases.
XX
PS Example 13; Fig 6C; 56pp; English.
XX
CC The invention relates to methods of detecting genetic deletions,
XX translocations and mutations associated with at least one condition
XX selected from the group consisting of DiGeorge syndrome (DGS),
XX CHARGE association, Velocardiofacial (Shprintzen) syndrome (VCF),
XX conotruncal defect and/or cleft palate in a human patient. DGS is
XX linked to chromosomal deletion of chromosome 22. The method
XX involves identifying in a sample DNA if there are less than 2
XX functional copies of chromosome 22q11 and including locus D22S36 to
XX locus BCR12, indicating a genetic deletion or mutation associated
XX with the conditions. The method is useful for diagnosing DGS, VCF,
XX CHARGE association, conotruncal defect and/or cleft palate,
XX particularly in prenatal monitoring. The present sequence is
XX der 22 DNA related to the invention.
XX
SQ Sequence 74 BP; 15 A; 27 C; 17 G; 15 T; 0 other;

```

Query Match 0.5%; Score 25.8; DB 24; Length 74;
 Best Local Similarity 60.9%; Pred. No. 3.1e+04; Mismatches 27; Indels 0; Gaps 0;
 Matches 42; Conservative 0;

```

QY 2764 CGCCGCTTCACGCAAGCCAGAGAGCGGCTGCCACGCTGCTACGCTACGCCC 2823
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4 CTCACCTTCCTCTCCACCTTCAGAGAGCGGCTGCAGGCGCATCATCTACAGGTCC 63
QY 2824 GCCCAGCAG 2832
   || ||| |
DB 64 TCCAAAGCTG 72

```

RESULT 28
 AAC21832
 ID AAC21832 standard; cDNA; 84 BP.
 XX
 AC AAC21832;

XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein 5' EST, SEQ ID NO: 25907.
 XX DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX KW gene therapy; chromosome mapping; ss.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-0200610.
 XX PR 26-FEB-1999; 99US-0122487.
 XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX DR WPI; 2000-500381/45.
 XX CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX SQ Sequence 84 BP; 15 A; 18 C; 23 G; 28 T; 0 other;
 XX
 Query Match 0.5%; Score 25.8; DB 21; Length 84;
 Best Local Similarity 67.9%; Pred. No. 3.2e+04;
 Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 4838 GGAGTTGAAGAGATTAACTGTTTGGCTGTTTGTAGTCTGTAT 4890
 DB 16 GGAGAGGAAGAATTTTACAGGCTTTTATTGGCGGTTATTTCTGTGTGT 68
 RESULT 29
 ID AAA36669
 XX AAA36669 standard; DNA; 97 BP.
 XX AC AAA36669;
 XX DT 01-AUG-2000 (first entry)
 XX DE RSV and PIV fusion protein F-RSV/HN-PIV3 oligonucleotide SEQ ID NO:28.
 XX DE RSV protein; heterochimeric; immunogenic; infection; RSV; PIV; MV;
 XX KW Muv; respiratory syncytial virus; parainfluenza virus; mumps virus;
 XX KW measles virus; glycoprotein; vaccine; immunisation; humanised; PCR;
 XX KW respiratory disorder; paramyxoviridae viral antigen; ss.
 XX OS Respiratory syncytial virus.
 XX OS Parainfluenza virus.

XX WO200018929-A2.
 XX PD 06-APR-2000.
 XX PF 20-SEP-1999; 99WO-EP07004.
 XX PR 25-SEP-1998; 98GB-0020931.
 XX PR 24-MAR-1999; 99GB-0006868.
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX XX Bollen A, Howard S;
 XX WPI; 2000-293163/25.
 XX DR
 XX CC Expressing viral (e.g. parainfluenza virus and measles virus)
 CC heterochimeric proteins comprising fragments of in Chinese Hamster
 CC Ovary cells, useful as vaccines for treating a human or animal
 CC susceptible to paramyxoviridae viral infections -
 XX Example 2; Fig 28; 127pp; English.
 XX CC The present invention describes a process for expressing, in Chinese
 CC Hamster Ovary (CHO) cells, a heterochimeric protein or its immunogenic
 CC derivative comprising immunogenic fragments of respiratory syncytial
 CC virus (RSV), parainfluenza virus type I (PIV1), PIV2, PIV3, measles
 CC virus (MV) or mumps virus (MuV) fusion and attachment glycoproteins.
 CC A vaccine comprising a protein as described above, can be used for
 CC treating a human or animal susceptible to paramyxoviridae viral
 CC infections. The heterochimeric proteins or their immunogenic derivatives
 CC are used in the manufacture of medicaments for use in the treatment of
 CC respiratory disorders. AAA36653 to AAA36695 represent oligonucleotides
 CC used in the generation of PCR fragments as part of the construction of
 CC an RSV/PIV3 fusion protein nucleotide sequence, and AAA36696 to AAA36699
 CC represent the RSV/PIV3 fusion protein nucleotide sequences produced in
 CC an example from the present invention. AAA36700 to AAA36739 represent
 CC oligonucleotides used in the generation of PCR fragments as part of the
 CC construction of an Muv/MV fusion protein nucleotide sequence, and
 CC AAA36740 to AAA36743 represent the nucleotide sequences produced in an
 CC example from the present invention.
 XX SQ Sequence 97 BP; 27 A; 35 C; 18 G; 17 T; 0 other;
 XX
 Query Match 0.5%; Score 25.8; DB 21; Length 97;
 Best Local Similarity 67.9%; Pred. No. 3.4e+04;
 Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 3098 GCCTGGCCCTCCCTGCTGTCGCCGCTTCAGCAGCTCAGCAGTCAACCCC 3150
 DB 18 GCCTGACCCCTCCCGAGGCTGACCTCTGCAACATCGACATCTTCAACCCC 70
 RESULT 30
 ID ABN36458
 XX ABN36458 standard; DNA; 60 BP.
 XX AC ABN36458;
 XX DT 15-JUL-2002 (first entry)
 XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:9206.
 XX DE Human; mouse; rat; splice transcript; detection; RNA transcript;
 XX KW splice variant; transcriptome; oligonucleotide library; ss.
 XX OS Homo sapiens.
 XX OS WO200210449-A2.
 XX PN 07-FEB-2002.
 XX PD 20-JUL-2001; 2001WO-IB01903.
 XX PF

[illegible]

```
PD XX 23-OCT-1997.
PF XX 04-APR-1997; 97WO-SE00574.
XX XX
PR 23-SEP-1996; 96SE-0003469.
PR 12-APR-1996; 96SE-0001422.
XX XX
PA (ASTR ) ASTRA AB.
XX XX
PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
XX XX
DR WPI; 1997-526397/48.
DR P-PSDB; AAW45007.
XX XX
PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)
PT which have immunostimulatory or immunosuppressive activity - can be
PT used to treat, e.g. cancers, infection, autoimmune disease or
PT transplant rejection
XX XX
PS Claim 14; Page 158; 183pp: English.
XX XX
CC The present sequence encodes an immunosuppressing or
CC immunostimulatory peptide. An immunosuppressant can be used to
CC treat transplant rejection or autoimmune disease, e.g. rheumatoid
CC arthritis, systemic lupus erythematosus, Sjogren's syndrome,
CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, Behcet's disease, type I diabetes,
CC Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
CC myasthenia gravis, encephalomyelitis, phemphigus vulgaris, vegetans
CC or foliaceus, Seneac-Usher syndrome or Brazilian pemphigus. An
CC immunostimulator can be used to treat conditions such as cancer or
CC infection.
XX XX
SQ Sequence 93 BP; 5 A; 29 C; 34 G; 25 T; 0 other;
XX XX
Query Match 0.5%; Score 25.6; DB 18; Length 93;
Best Local Similarity 62.5%; Pred. No. 3.7e+04;
Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX XX
QY 2580 CATGCTCAACAGGACAGCGCCAGCAGCCATCAGCTCGGCTACCTGAGCAGCG 2639
DB 69 CCTGCAAGCAGACAGGGCGACAGACCAGCAGCATGCGCGGACACCAGCAGCG 10
XX XX
QY 2640 CCGC 2643
DB 9 CAGC 6
XX XX
RESULT 35
AAV05449/c
ID AAV05449 standard; DNA; 93 BP.
XX XX
AC AAV05449;
XX XX
DT 27-APR-1998 (first entry)
XX XX
DE DNA for immunomodulatory peptide D22069AX.
XX XX
KW Immunomodulator; immunosuppressant; immunostimulator; treatment;
KW transplant rejection; autoimmune disease; cancer; infection; ss.
XX XX
OS Synthetic.
XX XX
FH Key Location/Qualifiers
FT mat_peptide 1..93
FT /*tag= a
FT /transl_except= (pos:66...68, aa:Arg)
XX XX
PN WO9739023-A1.
XX XX
PD 23-OCT-1997.
XX XX
PF 04-APR-1997; 97WO-SE00574.
XX XX
PR 23-SEP-1996; 96SE-0003469.
PR 12-APR-1996; 96SE-0001422.
XX XX
PA (ASTR ) ASTRA AB.
XX XX
PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
XX XX
DR WPI; 1997-526397/48.
DR P-PSDB; AAW45007.
XX XX
PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)
PT which have immunostimulatory or immunosuppressive activity - can be
PT used to treat, e.g. cancers, infection, autoimmune disease or
PT transplant rejection
XX XX
PS Claim 14; Page 158; 183pp: English.
XX XX
CC The present sequence encodes an immunosuppressing or
CC immunostimulatory peptide. An immunosuppressant can be used to
CC treat transplant rejection or autoimmune disease, e.g. rheumatoid
CC arthritis, systemic lupus erythematosus, Sjogren's syndrome,
CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, Behcet's disease, type I diabetes,
CC Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
CC myasthenia gravis, encephalomyelitis, phemphigus vulgaris, vegetans
CC or foliaceus, Seneac-Usher syndrome or Brazilian pemphigus. An
CC immunostimulator can be used to treat conditions such as cancer or
CC infection.
XX XX
SQ Sequence 93 BP; 5 A; 29 C; 34 G; 25 T; 0 other;
XX XX
Query Match 0.5%; Score 25.6; DB 18; Length 93;
Best Local Similarity 62.5%; Pred. No. 3.7e+04;
Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX XX
QY 2580 CATGCTCAACAGGACAGCGCCAGCAGCCATCAGCTCGGCTACCTGAGCAGCG 2639
DB 69 CCTGCAAGCAGACAGGGCGACAGACCAGCAGCATGCGCGGACACCAGCAGCG 10
XX XX
QY 2640 CCGC 2643
DB 9 CAGC 6
XX XX
RESULT 35
AAV05449/c
ID AAV05449 standard; DNA; 93 BP.
XX XX
AC AAV05449;
XX XX
DT 27-APR-1998 (first entry)
XX XX
DE DNA for immunomodulatory peptide D22069AX.
XX XX
KW Immunomodulator; immunosuppressant; immunostimulator; treatment;
KW transplant rejection; autoimmune disease; cancer; infection; ss.
XX XX
OS Synthetic.
XX XX
FH Key Location/Qualifiers
FT mat_peptide 1..93
FT /*tag= a
FT /transl_except= (pos:66...68, aa:Arg)
XX XX
PN WO9739023-A1.
XX XX
PD 23-OCT-1997.
XX XX
PF 04-APR-1997; 97WO-SE00574.
XX XX
PR 23-SEP-1996; 96SE-0003469.
PR 12-APR-1996; 96SE-0001422.
XX XX
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PA (ASTR) ASTRA AB.
 XX Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX WPI: 1997-526397/48.
 DR P-PSDB; AAW45017.
 XX Nucleic acids encoding cysteine- or methionine-containing peptide(s)
 PT which have immuno:stimulatory or immunosuppressive activity - can be
 PT used to treat, e.g. cancers, infection, auto:immune disease or
 PT transplant rejection
 XX Claim 14; Page 159; 183pp; English.
 XX The present sequence encodes an immunosuppressing or
 CC immunostimulatory peptide. An immunosuppressant can be used to
 CC treat transplant rejection or autoimmune disease, e.g. rheumatoid
 CC arthritis, systemic lupus erythematosus, Sjogren's syndrome,
 CC scleroderma, mixed connective tissue disease, dermatomyositis,
 CC polymyositis, Reiter's syndrome, Behcet's disease, type I diabetes,
 CC Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
 CC myasthenia gravis, encephalomyelitis, pemphigus vulgaris, vegetans
 CC or foliaceus, Seneur-Usher syndrome or Brazilian pemphigus. An
 CC immunostimulator can be used to treat conditions such as cancer or
 CC infection.
 XX Sequence 93 BP; 6 A; 30 C; 32 G; 25 T; 0 other;
 SQ Query Match 0.5%; Score 25.6; DB 18; Length 93;
 Best Local Similarity 62.5%; Pred. No. 3.7e+04;
 Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2580 CATGCTCAACAGAGGAGGAGCGGCGGACGATGCTCGGCTACCTGAGCAGCGG 2639
 Db 69 CTGCAAGGAGGAGGAGGCGGACGAGCGGCGGACGATGCTCGGCGGACGAGCGG 10
 QY 2640 CCGC 2643
 Db 9 CAGC 6

RESULT 37
 AAV05459/C
 ID AAV05459 standard; DNA; 93 BP.
 XX AC AAV05459;
 XX 27-APR-1998 (first entry)
 DE DNA for immunomodulatory peptide D22184AA.
 XX Immunomodulator; immunosuppressant; immunostimulator; treatment;
 KW transplant rejection; autoimmune disease; cancer; infection; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH mat_peptide 1..93
 FT /*tag= a
 FT
 XX WO9739023-A1.
 XX 23-OCT-1997.
 XX 04-APR-1997; 97WO-SE00574.
 XX 23-SEP-1996; 96SE-0003469.
 XX 12-APR-1996; 96SE-0001422.
 XX (ASTR) ASTRA AB.
 XX Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX WPI: 1997-526397/48.
 XX P-PSDB; AAW45015.
 XX Nucleic acids encoding cysteine- or methionine-containing peptide(s)

DR WPI: 1997-526397/48.
 DR P-PSDB; AAW45039.
 XX Nucleic acids encoding cysteine- or methionine-containing peptide(s)
 PT which have immuno:stimulatory or immunosuppressive activity - can be
 PT used to treat, e.g. cancers, infection, auto:immune disease or
 PT transplant rejection
 XX Claim 22; Page 163; 183pp; English.
 XX The present sequence encodes an immunosuppressing or
 CC immunostimulatory peptide. An immunosuppressant can be used to
 CC treat transplant rejection or autoimmune disease, e.g. rheumatoid
 CC arthritis, systemic lupus erythematosus, Sjogren's syndrome,
 CC scleroderma, mixed connective tissue disease, dermatomyositis,
 CC polymyositis, Reiter's syndrome, Behcet's disease, type I diabetes,
 CC Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
 CC myasthenia gravis, encephalomyelitis, pemphigus vulgaris, vegetans
 CC or foliaceus, Seneur-Usher syndrome or Brazilian pemphigus. An
 CC immunostimulator can be used to treat conditions such as cancer or
 CC infection.
 XX Sequence 93 BP; 6 A; 30 C; 34 G; 23 T; 0 other;
 SQ Query Match 0.5%; Score 25.6; DB 18; Length 93;
 Best Local Similarity 62.5%; Pred. No. 3.7e+04;
 Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2580 CATGCTCAACAGAGGAGGAGCGGCGGACGATGCTCGGCTACCTGAGCAGCGG 2639
 Db 69 CTGCAAGGAGGAGGAGGCGGACGAGCGGCGGACGATGCTCGGCGGACGAGCGG 10
 QY 2640 CCGC 2643
 Db 9 CAGC 6

RESULT 38
 AAV05456/C
 ID AAV05456 standard; DNA; 96 BP.
 XX AC AAV05456;
 XX 27-APR-1998 (first entry)
 DE DNA for immunomodulatory peptide D22045AX.
 XX Immunomodulator; immunosuppressant; immunostimulator; treatment;
 KW transplant rejection; autoimmune disease; cancer; infection; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH mat_peptide 1..96
 FT /*tag= a
 FT
 XX WO9739023-A1.
 XX 23-OCT-1997.
 XX 04-APR-1997; 97WO-SE00574.
 XX 23-SEP-1996; 96SE-0003469.
 XX 12-APR-1996; 96SE-0001422.
 XX (ASTR) ASTRA AB.
 XX Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX WPI: 1997-526397/48.
 XX P-PSDB; AAW45015.
 XX Nucleic acids encoding cysteine- or methionine-containing peptide(s)

PT which have immuno:stimulatory or immunosuppressive activity - can be
PT used to treat, e.g. cancers, infection, auto:immune disease or
PT transplant rejection

XX Claim 14; Page 159; 183pp; English.

XX The present sequence encodes an immunosuppressing or
CC immunostimulatory peptide. An immunosuppressant can be used to
CC treat transplant rejection or autoimmune disease, e.g. rheumatoid
CC arthritis, systemic lupus erythematosus, Sjogren's syndrome,
CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, Behcet's disease, type I diabetes,
CC Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
CC myasthenia gravis, encephalomyelitis, pemphigus vulgaris, vegetans
CC or foliaceus, Senebar-Usher syndrome or Brazilian pemphigus. An
CC immunostimulator can be used to treat conditions such as cancer or
CC infection.

XX Sequence 96 BP; 5 A; 30 C; 35 G; 26 T; 0 other;

Query Match 0.5%; Score 25.6; DB 18; Length 96;

Best Local Similarity 62.5%; Pred. No. 3.8e+04;

Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2580 CATGCTCAACAGAGGACAGAGCGCCAGCACCATCATCGCTGAGCAGCGC 2639

DB 69 CTTGAAGGCGACAGAGGCGAGAGCCAGCACCATCATCGCTGAGCAGCGC 10

QY 2640 CGCG 2643

DB 9 CAGC 6

RESULT 39

ABK43215

ID ABK43215 standard; DNA; 96 BP.

XX ABK43215;

XX 05-JUN-2002 (first entry)

XX Recombinant adenovirus fiber associated primer 418.

XX Modified virus; adenovirus; cytostatic; gene therapy; tumour cell;
XX proliferating cell; cancer; vascular disease; inflammatory disease;
XX infectious disease; human immunodeficiency virus; HIV; PCR; primer;
XX ss.

XX Synthetic.

XX WO200208263-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-GB03252.

XX 19-JUL-2000; 2000GB-0017720.

XX (GOTA-) GOT-A-GENE AB.

XX (GARD/) GARDNER R.

XX Lindholm L, Nord AK, Boulanger PA;

XX WPI; 2002-217049/27.

XX Novel modified virus comprising non-native polypeptides with stable
PT conformation and having framework moieties containing binding moieties
PT which confer upon the virus, an altered tropism, useful in gene therapy

XX Example 1; Page 46; 163pp; English.

XX The invention describes a modified virus comprising non-native

CC polypeptides which has framework moieties each containing binding
CC moieties, where the virus has altered tropism conferred by the binding
CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
CC of mammalian host cell in conformation which is maintained in absence of
CC ligands for the binding moieties, where the conformation allows the
CC binding moiety subsequently to bind with the ligand. The modified virus
CC is useful in therapy for the preparation of a medicament for treating
CC tumour cells, cancer, proliferating cells, vascular diseases,
CC inflammatory diseases and infectious diseases such as Human
CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
CC used in treatment of disease in human or animal subjects, either by in
CC vivo treatment of, or ex vivo treatment of cells of, the subject
CC requiring treatment. The problems associated with the expression of
CC functional non-native viral components in the nucleus and cytosol of
CC host cells is solved by using the modified virus for the purpose. This
CC sequence represents a primer associated with the creation of the
CC modified vector, described in the invention.

XX Sequence 96 BP; 8 A; 14 C; 10 G; 10 T; 54 other;

Query Match 0.5%; Score 25.6; DB 24; Length 96;

Best Local Similarity 26.6%; Pred. No. 3.8e+04;

Matches 25; Conservative 17; Mismatches 52; Indels 0; Gaps 0;

QY 2596 GACAGCAGCGCCAGCACCATCATCGCTGAGCAGCGCCGCTCTCAGGATC 2655

DB 2 GACTGCACCACTGGACCTGTSNNNSNNNSNNNSNNNSNNNSNNNSNNNS 61

QY 2656 TCGCCCTGCTTCTCCAGCGCCGCTCCAGCGAGG 2689

DB 62 NNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNS 95

RESULT 40

ABA72331/c

ID ABA72331 standard; DNA; 98 BP.

XX ABA72331;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #20636.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -

XX Claim 4; SEQ ID NO 20636; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for

CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 98 BP; 18 A; 18 C; 27 G; 35 T; 0 other;

Query Match 0.5%; Score 25.6; DB 22; Length 98;
 Best Local Similarity 62.5%; Pred. No. 3.8e+04;
 Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1861 AATGAGAAACCATATGTGTGCAAAATCCAGGCTGCACTAAGCGTTACACAGACCCCAAGC 1920
 || ||||| ||| ||||| ||| ||| ||| ||| ||||| |||||
 Db 95 AAACAGAAATCACAGATGTGCCAAACTCTGGGCATCTCACAGGGAGAGACAATGCCAAGC 36

Qy 1921 TCCC 1924

Db |||
 35 TCAC 32

Search completed: December 11, 2002, 02:41:53
 Job time : 664 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 19:50:51 ; Search time 638 Seconds
(without alignments)
17843.027 Million cell updates/sec

Title: US-09-910-185-3
Perfect score: 5055
Sequence: 1 cgtactactcgtggcattttt.....acccctctttttaaaaaaaaaa 5055

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5055	100.0	5055	ABK84036	Human cDNA differe
2	5055	100.0	5055	AA145547	Human Gli3 coding
3	3696.6	73.1	5113	AA145546	Murine Gli3 coding
4	366	7.2	557	ABQ15580	Oligonucleotide fo
5	366	7.2	557	ABQ15581	Oligonucleotide fo
6	334.8	6.6	3635	AA145541	Murine Gli1 coding
7	329.4	6.5	3326	AAF74625	Human Gli-1 nucleo
8	329.4	6.5	3600	AAD12302	Human Cubitus inte
9	329.4	6.5	3600	AA145542	Human Gli1 coding

10	329.4	6.5	3600	24	AA145543	Human Gli1 coding
11	329.4	6.5	3600	24	AA145544	Human Gli1 coding
12	329.4	6.5	3600	24	AA145545	Human Gli1 coding
13	329.4	6.5	3600	24	ABK30501	Human glioma-assoc
14	310.6	6.1	557	24	ABQ15578	Oligonucleotide fo
15	310.6	6.1	557	24	ABQ15579	Oligonucleotide fo
16	280.2	5.5	491	22	ABA59457	Human foetal liver
17	280.2	5.5	491	22	AA139286	Probe #7972 used t
18	280.2	5.5	491	24	ABS08369	Human genome-deriv
19	256	5.1	4853	23	ABL03987	Drosophila melanog
20	205	4.1	477	24	ABS08478	Human genome-deriv
21	204.6	4.0	462	24	ABS08520	Human genome-deriv
22	187.4	3.7	189	24	ABS20891	Human genome-deriv
23	185	3.7	185	24	ABS20932	Human genome-deriv
24	174.2	3.4	466	22	AAH99414	Human protein enco
25	171	3.4	2669	23	ABL08099	Drosophila melanog
26	167.8	3.3	470	22	ABA53823	Human foetal liver
27	167.8	3.3	470	22	AA133460	Probe #2146 used t
28	154	3.0	154	22	ABA71965	Human foetal liver
29	154	3.0	154	22	AA152336	Probe #21022 used
30	154	3.0	154	24	ABS20784	Human genome-deriv
31	124.4	2.5	10559	23	ABL03986	Drosophila melanog
32	122	2.4	124	22	ABA66401	Human foetal liver
33	122	2.4	124	22	AA146596	Probe #15282 used
34	113.4	2.2	6169	22	AA546369	Tumour suppressor
35	113.4	2.2	6169	24	ABN80096	Human chemically m
36	111.2	2.2	6169	22	AA546370	Tumour suppressor
37	111.2	2.2	6169	24	ABN80097	Human chemically m
38	110.4	2.2	1230	23	ABL06813	Drosophila melanog
39	109	2.2	3672	23	ABL06812	Drosophila melanog
40	102	2.0	2947	24	AB199239	Mouse ischaemic co
41	99.4	2.0	14486	22	AA527844	DNA encoding novel
42	93	1.8	2947	23	ABL02109	Drosophila melanog
43	90.8	1.8	3138	21	AAAG2683	Human Zicl gene.
44	90.8	1.8	3138	24	ABN95218	Gene #1716 used to
45	88.2	1.7	797	24	ABK34450	Human cDNA for nov

ALIGNMENTS

RESULT 1	
ABK84036	
ID	ABK84036 standard; cDNA; 5055 BP.
XX	
AC	ABK84036;
XX	
DT	14-AUG-2002 (first entry)
XX	
DE	Human cDNA differentially expressed in granulocytic cells #607.
XX	
KW	Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW	viral infection; parasitic infection; protozoal infection;
KW	fungal infection; sterile inflammatory disease; psoriasis;
KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW	adult respiratory distress syndrome; inflammatory bowel disease;
KW	Crohn's disease; ulcerative colitis; periodontal disease;
KW	granulocyte activation; chronic inflammation; allergy.
OS	Homo sapiens.
XX	
PN	WO200228999-A2.
XX	
PD	11-APR-2002.
XX	
PF	03-OCT-2001; 2001WO-US30821.
XX	
PR	03-OCT-2000; 2000US-237189P.
XX	
PA	(GENE-) GENE LOGIC INC.
XX	
PI	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

CC or a DNA encoding a Gli1 protein. The agents can be used in the
 CC prevention, treatment and diagnosis of bone and cartilage disorders
 CC including bone fractures, joint deformation, osteoarthritis,
 CC osteoporosis, cartilage damage, trauma, bone formation defects, cartilage
 CC formation defects, bone defects, dental disease, hyperosteoarthritis and
 CC hyperchondrogenesis, and for use in cosmetic and therapeutic bone
 CC transplantation. The present sequence is a human Gli3 coding sequence
 CC described in the exemplification of the invention.

XX Sequence 5055 BP; 1243 A; 1591 C; 1290 G; 931 T; 0 other;

SQ Query Match 100.0%; Score 5055; DB 24; Length 5055;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5055; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGATACAGTGGGCAATTTTGGTCCAGAGAGCTGAAGTAATGAGACACATCATGAG 60
 DB 1 CGATACAGTGGGCAATTTTGGTCCAGAGAGCTGAAGTAATGAGACACATCATGAG 60
 QY 61 GCCAGTCCACAGCTCCACGACCTGAAAGAAAAAGTTGAGAAATCCCATAGTGAAG 120
 DB 61 GCCAGTCCACAGCTCCACGACCTGAAAGAAAAAGTTGAGAAATCCCATAGTGAAG 120
 QY 121 TGCTCCACTCGACAGATGTGAGGAGAAAGCGTTGCCCTCCAGCACCACTTCTTAATGAG 180
 DB 121 TGCTCCACTCGACAGATGTGAGGAGAAAGCGTTGCCCTCCAGCACCACTTCTTAATGAG 180
 QY 181 GATGAAGTCTGGACAGACTTATACAGAGAGAGAGAAAGCAATCACTATGAGGCA 240
 DB 181 GATGAAGTCTGGACAGACTTATACAGAGAGAGAGAAAGCAATCACTATGAGGCA 240
 QY 241 CAGAATGTCCAGGGCTCAGCAAGTCACTGAGGACCTTCAACATCGAGTACAGAGAGG 300
 DB 241 CAGAATGTCCAGGGCTCAGCAAGTCACTGAGGACCTTCAACATCGAGTACAGAGAGG 300
 QY 301 GCCTCATTTGATCAAGAAAGATGCCATGGTCCCTGCCACAGCTGGGAGCGCTCTGTG 360
 DB 301 GCCTCATTTGATCAAGAAAGATGCCATGGTCCCTGCCACAGCTGGGAGCGCTCTGTG 360
 QY 361 CGGTACCGGGAGCGGTGTTGCAATGACACCGAGAAATGTTTACATGAGGCGCCACTAC 420
 DB 361 CGGTACCGGGAGCGGTGTTGCAATGACACCGAGAAATGTTTACATGAGGCGCCACTAC 420
 QY 421 CACCTCTCTCATCTTTCCCTGCTCCATCTCCATCTCCATTCGATGATGATGATGATGAT 480
 DB 421 CACCTCTCTCATCTTTCCCTGCTCCATCTCCATCTCCATTCGATGATGATGATGATGAT 480
 QY 481 GAGGCGGTTACCATTTACGATCCATCTCCGATTCCTCCATTCGATGATGATGATGATGAT 540
 DB 481 GAGGCGGTTACCATTTACGATCCATCTCCGATTCCTCCATTCGATGATGATGATGATGAT 540
 QY 541 TCTAGTAGGCTTACGATTCGAGGACCTGCGCTTCATTTAGGATTCGCCACACCGGACCC 600
 DB 541 TCTAGTAGGCTTACGATTCGAGGACCTGCGCTTCATTTAGGATTCGCCACACCGGACCC 600
 QY 601 GCTGCTGCTTCCAGTCTCCCTCAGCCCTCCACATCCCTACATTAATCCCTACATGGAC 660
 DB 601 GCTGCTGCTTCCAGTCTCCCTCAGCCCTCCACATCCCTACATTAATCCCTACATGGAC 660
 QY 661 TATATCCGCTTCCGATGACAGCCCATCGCTCCATGATCTCAGCAACCGGTGGGCTG 720
 DB 661 TATATCCGCTTCCGATGACAGCCCATCGCTCCATGATCTCAGCAACCGGTGGGCTG 720
 QY 721 AGCCCTACAGATGCGCCCATGAGGAGTACGCCAGAGATACATCATCATGATGGCC 780
 DB 721 AGCCCTACAGATGCGCCCATGAGGAGTACGCCAGAGATACATCATCATGATGGCC 780
 QY 781 CTGCTACTGCGCAGCGCCCTATGAGACATTAATCCCTCAGCTGCCACCGCCGCG 840
 DB 781 CTGCTACTGCGCAGCGCCCTATGAGACATTAATCCCTCAGCTGCCACCGCCGCG 840
 QY 841 ACGGGGCGCATCCACATGGAATATCTTCATGCTATGATGAGTACGACCATCTTCCAGCC 900
 DB 841 ACGGGGCGCATCCACATGGAATATCTTCATGCTATGATGAGTACGACCATCTTCCAGCC 900

DB 841 ACGGGGCGCATCCACATGGAATATCTTCATGCTATGATGAGTACGACCATCTTCCAGCC 900
 QY 901 AGGCTGTACAGCGCGAGCGGAGGACCTGCTCCATATCACCACCTCTCCGATCAT 960
 DB 901 AGGCTGTACAGCGCGGAGCGGAGGACCTGCTCCATATCACCACCTCTCCGATCAT 960
 QY 961 AGCTTTGACCTTCAGACCATGATAAGGACGCTCTCCCAACTCCTTTGGTCAAGATTTCAAT 1020
 DB 961 AGCTTTGACCTTCAGACCATGATAAGGACGCTCTCCCAACTCCTTTGGTCAAGATTTCAAT 1020
 QY 1021 AATTCCTAGCAGCTTTCAGCAAGTGGCTCCTATGCTCACTTATCTGCAAGTCAATC 1080
 DB 1021 AATTCCTAGCAGCTTTCAGCAAGTGGCTCCTATGCTCACTTATCTGCAAGTCAATC 1080
 QY 1081 AGCCTGCTTGTAGCTTACCTACTCTTCCGCGCGCTCTCTCCACATGCTCAGCAG 1140
 DB 1081 AGCCTGCTTGTAGCTTACCTACTCTTCCGCGCGCTCTCTCCACATGCTCAGCAG 1140
 QY 1141 ATCTTAAGCCGACACAGAGCTTAGGTTTACGCTTTGGACACAGCCCTCCACTCATCCAC 1200
 DB 1141 ATCTTAAGCCGACACAGAGCTTAGGTTTACGCTTTGGACACAGCCCTCCACTCATCCAC 1200
 QY 1201 CCTGCCCAACTTTTCCAAACACAGAGGCTATTCAGGGATTCCTACGGTTCTGAACCC 1260
 DB 1201 CCTGCCCAACTTTTCCAAACACAGAGGCTATTCAGGGATTCCTACGGTTCTGAACCC 1260
 QY 1261 GTCCAGTACGCTCGGCGCTTCTGAGTCTTCACAGAAAGCCCGACGAGTGTGCA 1320
 DB 1261 GTCCAGTACGCTCGGCGCTTCTGAGTCTTCACAGAAAGCCCGACGAGTGTGCA 1320
 QY 1321 GTGACGACCTGTGTGACCGCTGACAAAGAGGTTCCAAAGATCAAAACCCGATGAAGAC 1380
 DB 1321 GTGACGACCTGTGTGACCGCTGACAAAGAGGTTCCAAAGATCAAAACCCGATGAAGAC 1380
 QY 1381 CTCCCAAGCCGAGGCTCGGGGCGCAGGAGCAAGCCGAGGAAACACCTTTGTCAAG 1440
 DB 1381 CTCCCAAGCCGAGGCTCGGGGCGCAGGAGCAAGCCGAGGAAACACCTTTGTCAAG 1440
 QY 1441 GAGGAAGGGGCAAAAGATGAAAGCAACAGAGGCTGAGTCACTATGAGACAACTGC 1500
 DB 1441 GAGGAAGGGGCAAAAGATGAAAGCAACAGAGGCTGAGTCACTATGAGACAACTGC 1500
 QY 1501 CACTGGGAAGGCTCGGCGAGGAGTTTCGACACCAAGAGGAGCTTGTGACCATATAAT 1560
 DB 1501 CACTGGGAAGGCTCGGCGAGGAGTTTCGACACCAAGAGGAGCTTGTGACCATATAAT 1560
 QY 1561 AACGACCATATTCATGAGAGAAAGAGTTCGCTGTCAGGCTGGCTGAGTGTCAAGA 1620
 DB 1561 AACGACCATATTCATGAGAGAAAGAGTTCGCTGTCAGGCTGGCTGAGTGTCAAGA 1620
 QY 1621 GAGCAAGAACCTTCAAAGCCAGTATATGTTGTTAGTGCATATGAGAAAGACACCGGC 1680
 DB 1621 GAGCAAGAACCTTCAAAGCCAGTATATGTTGTTAGTGCATATGAGAAAGACACCGGC 1680
 QY 1681 GAGAAAGCTTCAAAATGCACTTTTGAAGTTGCAAAAGGCTTACTCGAGACTGAAAC 1740
 DB 1681 GAGAAAGCTTCAAAATGCACTTTTGAAGTTGCAAAAGGCTTACTCGAGACTGAAAC 1740
 QY 1741 TTGAAACACACTTTGAGATCTCACACTGAGAGAAACCATACGTTGTGAGCAGCAAGGT 1800
 DB 1741 TTGAAACACACTTTGAGATCTCACACTGAGAGAAACCATACGTTGTGAGCAGCAAGGT 1800
 QY 1801 TGCAACAGGCTTCTCAATGCTCTGATCGGCGCAACACCAACAGAACGATTC 1860
 DB 1801 TGCAACAGGCTTCTCAATGCTCTGATCGGCGCAACACCAACAGAACGATTC 1860
 QY 1861 AATGAAACCATATGTTGTGCAAAATCCAGCTGCATTAAGCGTTTACAGAGCCCAAGC 1920
 DB 1861 AATGAAACCATATGTTGTGCAAAATCCAGCTGCATTAAGCGTTTACAGAGCCCAAGC 1920
 QY 1921 TCCCTCCGGAACATGTGAAGACAGTGTGATGCGCCAGAGGCTCATGTCAACCAAGAGCAG 1980
 DB 1921 TCCCTCCGGAACATGTGAAGACAGTGTGATGCGCCAGAGGCTCATGTCAACCAAGAGCAG 1980

QY	1981	CGAGGGACATCCATCTCTCGCGGGCACCCCGAGAGATTCGGGAGCCATTCACAGTCC	2040
DB	1981	CGAGGGAGATCCATCTCTCGCGGGCACCCCGAGAGATTCGGGAGCCATTCACAGTCC	2040
QY	2041	AGTGCCTTGGCGACCGACTCAGGAGGCCCTTGTGTAGCAGCAGGACCTCAGCAACACT	2100
DB	2041	AGTGCCTTGGCGACCGACTCAGGAGGCCCTTGTGTAGCAGCAGGACCTCAGCAACACT	2100
QY	2101	ACCTCAAAGCGGGAAGTSCCTCCAGGTGAAACCGTCAAGGCAGAGAGCCAAATGACA	2160
DB	2101	ACCTCAAAGCGGGAAGTSCCTCCAGGTGAAACCGTCAAGGCAGAGAGCCAAATGACA	2160
QY	2161	TCACGCAAGCCCTGGTGGTCAGTCTTCATGTACAGCAGCCAAACAGTCCCCCATCAGCAAC	2220
DB	2161	TCACGCAAGCCCTGGTGGTTCAGTCTTCATGTACAGCAGCCAAACAGTCCCCCATCAGCAAC	2220
QY	2221	TATTTCAAACAGTGGGTCGAGCTTCCTCTGACCGATGAGGTACTATAGGAGACCTCAGT	2280
DB	2221	TATTTCAAACAGTGGGTCGAGCTTCCTCTGACCGATGAGGTACTATAGGAGACCTCAGT	2280
QY	2281	GCCATCGATGAAACCCCAATCATGTGACTCAACATTTCCACTGTGCAACACAGACCCCTTGCT	2340
DB	2281	GCCATCGATGAAACCCCAATCATGTGACTCAACATTTCCACTGTGCAACACAGACCCCTTGCT	2340
QY	2341	TTGCAAGCAGAGAAACCCGCGAGGACCAATGTGATGGAGCAGCTAAACCTAGAAAGG	2400
DB	2341	TTGCAAGCAGAGAAACCCGCGAGGACCAATGTGATGGAGCAGCTAAACCTAGAAAGG	2400
QY	2401	CTAAACAAGTGAATGTAATTTCCGCGACTGAAACCCATTTCTACCCCTTAAGGCCCT	2460
DB	2401	CTAAACAAGTGAATGTAATTTCCGCGACTGAAACCCATTTCTACCCCTTAAGGCCCT	2460
QY	2461	CGGCTCTCTCTCATAGGAAATGGCACACAGCTCCAAACACACTGCAGCTTGGGTGGG	2520
DB	2461	CGGCTCTCTCTCATAGGAAATGGCACACAGCTCCAAACACACTGCAGCTTGGGTGGG	2520
QY	2521	CCCATGACGCTTCTCCCGGCGAGACGACCTCTCTGGGTGGAGCTCATATGCTGTAAC	2580
DB	2521	CCCATGACGCTTCTCCCGGCGAGACGACCTCTCTGGGTGGAGCTCATATGCTGTAAC	2580
QY	2581	ATGCTCAACAGAAAGGACAGCAGCGCCAGCACCATCAGCTCGCGCTTACCTGAGCAGCCG	2640
DB	2581	ATGCTCAACAGAAAGGACAGCAGCGCCAGCACCATCAGCTCGCGCTTACCTGAGCAGCCG	2640
QY	2641	CGCTCTCAGGAGTCTCGCCCTGCTTCTCAGCGCGCTCCACGAGGCGTCCACAGGC	2700
DB	2641	CGCTCTCAGGAGTCTCGCCCTGCTTCTCAGCGCGCTCCACGAGGCGTCCACAGGC	2700
QY	2701	GAGGCGGCGCGCAAGACGTGAGCGTGGCGACTCTTACGACCCCATCTCCACCGAGCC	2760
DB	2701	GAGGCGGCGCGCAAGACGTGAGCGTGGCGACTCTTACGACCCCATCTCCACCGAGCC	2760
QY	2761	TCGCGCGCTTCCAGGGAAGCCAGCCAGCAGCGCCTTCCCGACCTGCTCAGCCTCAGG	2820
DB	2761	TCGCGCGCTTCCAGGGAAGCCAGCAGCGCCTTCCCGACCTGCTCAGCCTCAGG	2820
QY	2821	CCGCGCCAGAGTACCGCTCAAGGCCAAGTACGCGGCTGCCACAGAGGGCGCGCGCG	2880
DB	2821	CCGCGCCAGAGTACCGCTCAAGGCCAAGTACGCGGCTGCCACAGAGGGCGCGCGCG	2880
QY	2881	ACGCCCTGCCCAACATGGAGAGGATGAGCCTGAAGACGCGCCTTGGCGCTGCTCGGGGAT	2940
DB	2881	ACGCCCTGCCCAACATGGAGAGGATGAGCCTGAAGACGCGCCTTGGCGCTGCTCGGGGAT	2940
QY	2941	GCCTCGAGCCTTGGGCTGGCCCTGCCTCCAGTTTCATGCCCGAGGAGGTGCAGCAGCGG	3000
DB	2941	GCCTCGAGCCTTGGGCTGGCCCTGCCTCCAGTTTCATGCCCGAGGAGGTGCAGCAGCGG	3000
QY	3001	GGAGCCACGGCTACGGGGCGGCCACTCTGACCGCGACGATGCGCTGGGCCACGCGCTG	3060
DB	3001	GGAGCCACGGCTACGGGGCGGCCACTCTGACCGCGACGATGCGCTGGGCCACGCGCTG	3060

Qy	3061	AGAGGGCCAGCGACCCCGGTGCGGACAGGCTCCGAGGGCCCTGGCCCTGCTGTGTGCCG	3120
Db	3061	AGGAGGGCCAGCGACCCCGGTGCGGACAGGCTCCGAGGGCCCTGGCCCTGCTGTGTGCCG	3120
	3121	CGCTTCAGCAGCCTCAGCAGCTGCACACCCCGCGGATGCGCCAGTCCGCGGAGACGCG	3180
Db	3121	CGCTTCAGCAGCCTCAGCAGCTGCACACCCCGCGGATGCGCCAGTCCGCGGAGACGCG	3180
Qy	3181	AGTCTCGTCTTCAGAAATTCACACGCGGCCCGAGGGCGGCCAGTCCCGAAACTTCCACTCG	3240
Db	3181	AGTCTCGTCTTCAGAAATTCACACGCGGCCCGAGGGCGGCCAGTCCCGAAACTTCCACTCG	3240
Qy	3241	TTCCCTGTGCTCTCCAGCATCACCGAGAACGTCAACCTTGGAGTCCCTTGACCATGGACGCT	3300
Db	3241	TTCCCTGTGCTCTCCAGCATCACCGAGAACGTCAACCTTGGAGTCCCTTGACCATGGACGCT	3300
Qy	3301	GATGCCAACCTGACGATCAGGATTTCTTCCGCGGACGACGTGTGTGCAGTATTTAAATTCC	3360
Db	3301	GATGCCAACCTGACGATCAGGATTTCTTCCGCGGACGACGTGTGTGCAGTATTTAAATTCC	3360
Qy	3361	CAGAAACAAGCAGGGTACGAGCAGCACTTCCCCAGCGCCCTCCCGGACGACAGCAAGTG	3420
Db	3361	CAGAAACAAGCAGGGTACGAGCAGCACTTCCCCAGCGCCCTCCCGGACGACAGCAAGTG	3420
Qy	3421	CCCCACGGGCCGGTGACTTTGACGCGCCCGGGTGCCAGACAGCCACGCTGCCACGACAG	3480
Db	3421	CCCCACGGGCCGGTGACTTTGACGCGCCCGGGTGCCAGACAGCCACGCTGCCACGACAG	3480
Qy	3481	TTCCATGCCCTTGAGCAGGCCCTGCCCGCAGGGCAGCAAAACCGACCTGCCCNTTCAGTGG	3540
Db	3481	TTCCATGCCCTTGAGCAGGCCCTGCCCGCAGGGCAGCAAAACCGACCTGCCCNTTCAGTGG	3540
Qy	3541	AACGAAGTCAGTCCGGAAGCGCGACCTGTCTCTCCAAGCTCAAGTGTGGCGCGCGG	3600
Db	3541	AACGAAGTCAGTCCGGAAGCGCGACCTGTCTCTCCAAGCTCAAGTGTGGCGCGCGG	3600
Qy	3601	CCGCGTGTGCCGACAGCTCGCCCTTTGGTGTCTGCAACGCATGTGTCTCCACCCGCGAG	3660
Db	3601	CCGCGTGTGCCGACAGCTCGCCCTTTGGTGTCTGCAACGCATGTGTCTCCACCCGCGAG	3660
Qy	3661	AACCCCTTGAGGAGCGGCCCTGCTGGGGGCTATCAGACCCCTCGGGGAGAACACGCAACCC	3720
Db	3661	AACCCCTTGAGGAGCGGCCCTGCTGGGGGCTATCAGACCCCTCGGGGAGAACACGCAACCC	3720
Qy	3721	TACGGTGGCCACAGACACTTGATGTCTCCACAACGCCCGGAACTGCACACAGTGGAAAC	3780
Db	3721	TACGGTGGCCACAGACACTTGATGTCTCCACAACGCCCGGAACTGCACACAGTGGAAAC	3780
Qy	3781	GCCTTCCATGAACAGCCCTGTAAAGCCCGCGAGTATGGAACCTGTCTCAACAGCGAGCCA	3840
Db	3781	GCCTTCCATGAACAGCCCTGTAAAGCCCGCGAGTATGGAACCTGTCTCAACAGCGAGCCA	3840
Qy	3841	GTGGCCCTTGTTGCACTCGACGGTGCTGTGGTCCGGGATTCAGCCTCAAAGCTGAAG	3900
Db	3841	GTGGCCCTTGTTGCACTCGACGGTGCTGTGGTCCGGGATTCAGCCTCAAAGCTGAAG	3900
Qy	3901	AGCACCCCATGCAAGGAGCGGGGCCAGCTGAATTTCCGCTGCCGGTAGCGCCAAAT	3960
Db	3901	AGCACCCCATGCAAGGAGCGGGGCCAGCTGAATTTCCGCTGCCGGTAGCGCCAAAT	3960
Qy	3961	GAGTCAGCTGGCAGCATGTGAATGGCATGCAAGACACGAGCACCGGAGCGCGGTAC	4020
Db	3961	GAGTCAGCTGGCAGCATGTGAATGGCATGCAAGACACGAGCACCGGAGCGCGGTAC	4020
Qy	4021	CTGGCTCACCAAGCTCCTCGGGCAGAGATGACGACCCCGGGGAGCGCCGCCCGGTCTAG	4080
Db	4021	CTGGCTCACCAAGCTCCTCGGGCAGAGATGACGACCCCGGGGAGCGCCGCCCGGTCTAG	4080
Qy	4081	CAGATCTTTGGCAGATTAGTGTCTACCTTCACATCAACATCTACCAAGGCCCAGAGAGC	4140
Db	4081	CAGATCTTTGGCAGATTAGTGTCTACCTTCACATCAACATCTACCAAGGCCCAGAGAGC	4140
Qy	4141	TGCTTCCACAGGGGCTCAGGGCATGGGACGACCGCTCAAGCTTGGCAGTTGTCAAGGGC	4200

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Db 4141 TGCTGCCAGGGGCTCAGGCGATGGCAGCCAGCCGCTCAAGCTGGCAGTTGTCCAGGGC 4200
QY 4201 TACAGCCCATGTGCAGCTTTGGGGGCGAGCAGGGCCAGGTATGCCAGGAGACAGCCTT 4260
Db 4201 TACAGCCCATGTGCAGCTTTGGGGGCGAGCAGGGCCAGGTATGCCAGGAGACAGCCTT 4260
QY 4261 GCTCTGCAGTCAGGACAGCTCAGTCAGACCAAGTCAGAGCCTGCAGGGTGAATGGTATCAAG 4320
Db 4261 GCTCTGCAGTCAGGACAGCTCAGTCAGACCAAGTCAGAGCCTGCAGGGTGAATGGTATCAAG 4320
QY 4321 ATGGAGATGAAGAGGCGAGCCCATCGCTGTCTTAATCTGCAGAAATTAATCTGTGTCAG 4380
Db 4321 ATGGAGATGAAGAGGCGAGCCCATCGCTGTCTTAATCTGCAGAAATTAATCTGTGTCAG 4380
QY 4381 TTCTATGACCAAAACCGTGGGCTTTCAGTCAGCAAGACAGAAAGCTGGTTCATCTCTATT 4440
Db 4381 TTCTATGACCAAAACCGTGGGCTTTCAGTCAGCAAGACAGAAAGCTGGTTCATCTCTATT 4440
QY 4441 TCAGAGCCGAGCTGCTGTCTACAGGGGACCGCCAGCCCAAAACTCTGAGTTACTTTCCCCA 4500
Db 4441 TCAGAGCCGAGCTGCTGTCTACAGGGGACCGCCAGCCCAAAACTCTGAGTTACTTTCCCCA 4500
QY 4501 GGTGCTAATCAGGTGACAGCAGCTGGACAGCCCTCGACAGCCATGACCTGGAAGGGGTA 4560
Db 4501 GGTGCTAATCAGGTGACAGCAGCTGGACAGCCCTCGACAGCCATGACCTGGAAGGGGTA 4560
QY 4561 CAGATTGACTTCGATGCCCATATAGACGATGGGGACCACTCCAGCCTGATGTCGGGGGCC 4620
Db 4561 CAGATTGACTTCGATGCCCATATAGACGATGGGGACCACTCCAGCCTGATGTCGGGGGCC 4620
QY 4621 CTCAGCCCAAGTATCATTCAGAACCTTTCCCATAGCTCTCCCGCCTCACCACGCTCGG 4680
Db 4621 CTCAGCCCAAGTATCATTCAGAACCTTTCCCATAGCTCTCCCGCCTCACCACGCTCGG 4680
QY 4681 GGTGCTCCTCCCATTCAGCTGCTGTCCATGAGCACCACCAACATGGCTATCGGGGACAT 4740
Db 4681 GGTGCTCCTCCCATTCAGCTGCTGTCCATGAGCACCACCAACATGGCTATCGGGGACAT 4740
QY 4741 GAGTTCTTTGCTGACCTCCCTAGCGGAGAAAGCAAAATTCCTTGCAATGCAATAGGC 4800
Db 4741 GAGTTCTTTGCTGACCTCCCTAGCGGAGAAAGCAAAATTCCTTGCAATGCAATAGGC 4800
QY 4801 TTTAGAAAAAAGACTGCAACCAACGGAATCAATAGGAGTTGAAGAGATTAAACTGAC 4860
Db 4801 TTTAGAAAAAAGACTGCAACCAACGGAATCAATAGGAGTTGAAGAGATTAAACTGAC 4860
QY 4861 TTTGTTTGGCTGTTTTTTTAGTTCTGTATGTTTTAGCAATCTCATCTCACTTAAGTATTC 4920
Db 4861 TTTGTTTGGCTGTTTTTTTAGTTCTGTATGTTTTAGCAATCTCATCTCACTTAAGTATTC 4920
QY 4921 AGATGTTTCAATATATATTTTATGGAAGAGACTCTGAAAAACCTTAAGTATTC 4980
Db 4921 AGATGTTTCAATATATATTTTATGGAAGAGACTCTGAAAAACCTTAAGTATTC 4980
QY 4981 TAGGGAGAAACTGCTCTCCATTTTCAGTTTGAATCAGTATTTTACACTCAACACACCT 5040
Db 4981 TAGGGAGAAACTGCTCTCCATTTTCAGTTTGAATCAGTATTTTACACTCAACACACCT 5040
QY 5041 CTTTTTAAAAA 5055
Db 5041 CTTTTTAAAAA 5055

RESULT 3
ID AAL45546
CDNA: 5113 BP.
XX AAL45546 standard;
XX AAL45546;
XX 11-JUN-2002 (first entry)
XX Murine Gli3 coding sequence SEQ ID NO: 20.

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XX Gli1: screening method; bone induction; cartilage induction;
KW orthopaedic disease; dental disease; osteoporosis; hyperosteoegenesis;
KW osteopathic; antiarthritic; vulnary; immunosuppressive;
KW hyperchondrogenesis; mouse; gene; ss.
XX MUS SP.
OS
XX Key Location/Qualifiers
FH 172..4962
FT CDS /*tag= a
FT /product= "Gli3"
FT /note= "q"
XX W0200211752-A1.
PN
XX 14-FEB-2002.
PD
XX 03-AUG-2001; 2001WO-JP06688.
PF
XX 04-AUG-2000; 2000JP-0242767.
PR
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Hikichi Y;
PI
XX WPI; 2002-241709/29.
DR P-PSDB; AAO17113.
XX
XX Promotion of bone and cartilage formation using Gli1 protein or DNA
XX encoding it for treatment of skeletal disorders
XX
XX Disclosure; Page 133-136; 154pp; Japanese.
XX
XX The present invention relates to agents for the promotion of bone and
XX cartilage formation which contain as the active component a Gli1 protein
XX or a DNA encoding a Gli1 protein. The agents can be used in the
XX prevention, treatment and diagnosis of bone and cartilage disorders
XX including bone fractures, joint deformation, osteoarthritis,
XX osteoporosis, cartilage damage, trauma, bone formation defects, cartilage
XX formation defects, bone defects, dental disease, hyperosteoegenesis and
XX hyperchondrogenesis, and for use in cosmetic and therapeutic bone
XX transplantation. The present sequence is a murine Gli3 coding sequence
XX described in the exemplification of the invention.
XX
XX Sequence 5113 BP; 1337 A; 1490 C; 1254 G; 1032 T; 0 other;
XX
Query Match 73.1%; Score 3696.6; DB 24; Length 5113;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 4212; Conservative 0; Mismatches 769; Indels 24; Gaps 3;
QY 9 CGTGGGCAATTTTGGTCGAAGAGAGCTGAAGTAATGAGACATCATGAGGCCAGTC 68
Db 126 CGCAGGGATTCCTTTGAGAAAACAAGCTGAAGTAATGAGACATTTATGGAGGCCAGGC 185
QY 69 CCACAGCTCCACGACCACTGAAAAGAAAAGTTGAGAAATTCATAGTGAAGTCTCCAC 128
Db 186 CCACAGCTCTACGGGACTGAGAGAGAGAAAGCTGAAATTCATTTGGAAATGCTCCAC 245
QY 129 TCGAACAGATGTGAGCGAGAGAAAGCGTTGCTCCAGCACCACCTTCTTAATGAGGATGAAG 188
Db 246 GAGAACAGATCTCAGCGAGAGAGCGCTGCTCTAGTACCCTTCCAATGAGGATGAAG 305
QY 189 TCCTGGACAGACTTATCAGACAGAGAGAGAAAGCAATCACTATGAGCCACAGATGT 248
Db 306 TCCTGGACAGACTTATCAGCGAGAGAGAAAGCAATCACTATGAGCCCTCAGAGTGT 365
QY 249 CCAGGGCTCAGCAAGATCAGTGAGGAGACCTTCAACATCGAGTCAGAGAGGGCTCATT 308
Db 366 GCAGGGTCTCAACAAATCAGTGAGGAGCCCTCGACGCTCTAGTATGAGAGGGCTCGCT 425
QY 309 GATCAAGAAAGAGATCCATGGTCCCTGCGCACAGTGGCGGAGCCCTCTGTGCGGTACCG 368

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[illegible]

Db 4806 ATCCCTCCATCCCAATCCCTATCCATGGGCGACCAACACATGGCTATCGGGATATGA 4865
 Qy 4743 GTTCCTTCTGCTGACCTCCCTAGCGAAGAACAAATTCCTTGCAGTTATGCAATAGGCTT 4802
 Db 4866 GTTCCTTCTGCTGACCTCCCTTCGAGAAGAACAAAGTTCTTGCAGTTATGCAATAGGCGG 4925
 Qy 4803 TAGGAAAAAAGACTGCAACCAACGGAATCAATAGGAGTTGAAGAGATTAAATGACTT 4862
 Db 4926 TAGGCAAGAGGACCAACCAACAAAGACTGAATGACTTGGGA----- 4969
 Qy 4863 TGTTCCTGCTGTTTTTTTAGTTCGTATGTAATTTAGCAATCTCATCTCACTCACTAG 4922
 Db 4970 -TTTTTTTTTCTTTTAAAGTCTGCTGTAATTTAGCAATCTCATCTCACTCACTAGG 5028
 Qy 4923 ATGCTGTTCAATATATTCCTTTTATGAAAAGGACTCTGAAAACCTTAAGTATCTA 4982
 Db 5029 ATGCTGTCGAAGTATATTCCTTTTATGAAAAGGACTCTGAAAACCTTAAGTATCTA 5088
 Qy 4983 -GGGAGAAACTGCTTCCATTTTCAG 5006
 Db 5089 GGGGAGAACTGCTTCCATTTTCAG 5113

RESULT 4
 ABQ15580/C
 ID ABQ15580 standard; DNA; 557 BP.
 XX
 AC ABQ15580;
 XX
 12-JUL-2002 (first entry)
 XX
 Oligonucleotide for detecting cytosine methylation SEQ ID NO 2171.
 XX
 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 drug; side effect; cancer; central nervous system; cardiovascular;
 gastrointestinal; respiratory system; single nucleotide polymorphism;
 SNP; cell differentiation; ds.
 XX
 Homo sapiens.
 XX
 WO200218632-A2.
 XX
 07-MAR-2002.
 XX
 01-SEP-2001; 2001WO-EPI0074.
 XX
 01-SEP-2000; 2000DE-1043826.
 XX
 05-SEP-2000; 2000DE-1044543.
 XX
 (EPIG-) EPIGENOMICS AG.
 XX

Olek A, Piepenbrock C, Berlin K, Guetig D;
 WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful
 for diagnosis and prognosis, comprises selective hybridization of
 amplicons from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of
 methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 genomic sample of DNA. The sample is treated chemically to convert
 cytosine (C) but not methylated C, to uracil, then part of the genomic
 DNA that contains the target C is amplified to form a labeled amplicon.
 The amplicon is hybridised to two classes, each with at least one
 member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 and the degree of hybridisation to both classes is determined from the
 label on the amplicon. From the ratio of labels hybridised to the two
 classes of oligomers, the degree of methylation is calculated. The method
 is used: (i) for diagnosis and/or prognosis of side effects of
 therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders

CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.

XX Sequence 557 BP; 75 A; 52 C; 205 G; 225 T; 0 other;

Query Match 7.2%; Score 366; DB 24; Length 557;
 Best Local Similarity 79.1%; Pred. No. 2.4e-72;
 Matches 435; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 2989 TGACGACGGGGAGGCCACGCTAGCGGGCGGCCACCTGCGAGCGGCACGATGGCGTG 3048
 Db 552 TACACGACGAAAAAACCCACGACTACGAGCAGCGCCACTACACCCGCGATACGCGG 493

Qy 3049 GGCACGCGGTGAGGAGGCCAGCGCCGCTCGCAGCAGGCTCCGAGGGCCCTGGGCCCTG 3108
 Db 492 AACACGACGTAAAAAACCCACGACCGCCGATACGACAACTCCGAAAACTTAACCTTA 433

Qy 3109 CCTCGTGTGCGCGCTTACGACGCTTACGAGCTGCAACCCCGCGCGGCGCCAGTCC 3168
 Db 432 CCTCGTATACCGCGCTTCAACAACTCAACAACTACAAACCCCGCGACGATACCGTCC 373

Qy 3169 GCGGAGAACGCGAGTCTCGTCTCAGAAATACAGCGGCGCGCGCGCCAGTCCCGA 3228
 Db 372 GCGAAAAACGCAATCTCGTACTTCAAAATACACGCGCCCGGAAAAACGACCAATCCCGA 313

Qy 3229 AACTTCCACTCTGCTCCCTCTCTCCAGCATCAGCGAAGACGTCACCTTGGAGTCCCTG 3288
 Db 312 AACTTCCACTCTGCTCCCTCTCTCCAGCATCAGCGAAGACGTCACCTTAAATCCCTA 253

Qy 3289 ACCATGACGCTGATGCTCAACCTGAAAGATGAGGATTTCTGCGGACGACGTGGTGAC 3348
 Db 252 ACCATAAACGCTAATACCAACCTAAAGATATAAATTTCTTACCGAACGACGTAATACAA 193

Qy 3349 TATTTAAATTCCTCAGAACGAGGCTACGAGCAGCTTCCCGCGCGCTCCCGGAC 3408
 Db 192 TATTTAAATTCCTCAGAACGAGGCTACGAGCAGCTTCCCGCGCGCTCCCGGAC 133

Qy 3409 GACAGCAAGTGCCTCCCGCGCGCTGACTTTGACGCGCGCGGCTGCGACAGCCAC 3468
 Db 132 GACACAAAATACCCACGAAACCGATACTTTAAGCGCGCGCGGAACTTACCAAAACACCA 73

Qy 3469 GCTGGCCGACGATTCATGCTGCGGACGCTGCGGCGCGCGGCGGCGGCGGCGGCGG 3528
 Db 72 GCTAACCAACAATTCATACCTCTCGAACACCTTACCCCGGAAAAACAAACAAACCGACCTA 13

Qy 3529 CCCATTTCAGT 3538
 Db 12 CCCATTTCAT 3

RESULT 5
 ABQ15581
 ID ABQ15581 standard; DNA; 557 BP.

XX
 AC ABQ15581;
 XX

12-JUL-2002 (first entry)
 XX

Oligonucleotide for detecting cytosine methylation SEQ ID NO 2172.
 XX

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 drug; side effect; cancer; central nervous system; cardiovascular;
 gastrointestinal; respiratory system; single nucleotide polymorphism;
 SNP; cell differentiation; ds.
 XX

Homo sapiens.
 XX

PN WO200218632-A2.
 XX 07-MAR-2002.
 XX 01-SEP-2001; 2001WO-EP10074.
 XX 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K, Guetig D;
 PI WPI; 2002-371829/40.
 DR
 XX
 XX Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA
 PS
 XX Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ARQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 XX
 XX Sequence 557 BP; 225 A; 205 C; 52 G; 75 T; 0 other;
 SQ
 Query Match 7.2%; Score 366; DB 24; Length 557;
 Best Local Similarity 79.1%; Pred. No. 2.4e-72;
 Matches 435; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
 QY 2989 TGCAGGCGAGGGGAGCCACGCGTACGGGGCGGCGCCACCTGCGAGCGGCGTGGCCCTG 3048
 DB 6 TACACGACGAGAAACCCACGACTACGACGCGCCCTACACCGCGCATACGCGG 65
 QY 3049 GGCACGCGGTGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3108
 DB 66 AACGACGAGTAAACAAACACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 125
 QY 3109 CTTGCTGCTGCGGCGGCTTACGAGCGCTGACGAGCTGCAACCGCGGCGGCGGCGGCGGCGG 3168
 DB 126 CTTGCTGATACCGGCTTCAACACCTCAACAACTCAACACCGCGGCGGCGGCGGCGGCGG 185
 QY 3169 GCGGAGACGCGAGTCTGCTGCTTACAGATTACACGCGGCGGCGGCGGCGGCGGCGGCGG 3228
 DB 186 GCGAAACGCGAATCTCTGCTTCAAAATACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245
 QY 3229 AACTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3288
 DB 246 AACTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
 QY 3289 ACATGAGCGCTGATGCGCAACCTGACGATGAGGATTCTCTGCGGAGCAGCTGTGTGCGAG 3348
 DB 306 ACCATAACGCTAATACCAACCTAAACGATAAAATTTCTACCGAAGCAGCTAATACAA 365
 QY 3349 TATTTAAATCCAGNACCAACGAGGTACGAGCAGCTTCCCGAGCGCCCTCCCGGAC 3408

Db 366 TATTTAAATCCCAAAACCAAAATACGAAACAACTTCCCAACGCGCTCCCGAAC 425
 QY 3409 GACAGCAAAAGTCCCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3468
 Db 426 GACAACAAAATACCCGACGAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 485
 QY 3469 GCTGGCCAGCAGTTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3528
 Db 486 GCTAACCAAAATTCATACCTCGAACACCTTACCCCGAAACAAACAAACCGGCGGCGG 545
 QY 3529 CCCATTTCAGT 3538
 Db 546 CCCATTTCAGT 555
 RESULT 6
 AAL45541
 ID AAL45541 standard; cDNA; 3635 BP.
 XX
 AC AAL45541;
 XX
 DT 11-JUN-2002 (first entry)
 XX
 DE Murine Gli1 coding sequence SEQ ID NO: 9.
 XX
 KW Gli1; screening method; bone induction; cartilage induction;
 KW orthopaedic disease; dental disease; osteoporosis; hyperosteoecgenesis;
 KW osteoarthritis; antiarthritic; vulnary; immunosuppressive; human;
 KW hyperchondrogenesis; gene; mouse; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..3548
 FT /*tag= a
 FT /product= "Gli1"
 FT
 XX WO200211752-A1.
 XX
 PD 14-FEB-2002.
 XX
 XX 03-AUG-2001; 2001WO-JP06688.
 XX
 PR 04-AUG-2000; 2000JP-0242767.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Hikichi Y;
 XX
 DR WPT; 2002-241709/29.
 DR P-PSDB; AAO17108.
 PT
 PT Promotion of bone and cartilage formation using Gli1 protein or DNA
 encoding it for treatment of skeletal disorders
 XX
 PS Claim 6; Page 88-89; 154pp; Japanese.
 XX
 CC The present invention relates to agents for the promotion of bone and
 CC cartilage formation which contain as the active component a Gli1 protein
 CC or a DNA encoding a Gli1 protein. The agents can be used in the
 CC prevention, treatment and diagnosis of bone and cartilage disorders
 CC including bone fractures, joint deformation, osteoarthritis,
 CC osteoporosis, cartilage damage, trauma, bone formation defects, cartilage
 CC formation defects, bone defects, dental disease, hyperosteoecgenesis and
 CC hyperchondrogenesis, and for use in cosmetic and therapeutic bone
 CC transplantation. The present sequence is a murine Gli1 coding sequence
 CC described in the exemplification of the invention.
 XX
 SQ Sequence 3635 BP; 786 A; 1140 C; 989 G; 719 T; 1 other;
 Query Match 6.6%; Score 334.8; DB 24; Length 3635;
 Best Local Similarity 70.4%; Pred. No. 4.9e-65;

Matches 463; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 1336 GACCGATGACACAAAGAGGTCCAAAGATCAAAACCCGATGAAGACTCCCGAGCCAGGG 1395
 Db 771 GATATGATGTTGGCAAGTGGCCGAGGACCTTTGGAAAGGGACATCTTAGCCCCAAC 830
 QY 1396 GCTCGGGGCGACAGACAGCCCGAAGCAACACCCCTTGTCAAGGAGGAGGGACAAA 1455
 Db 831 TCCACAGGCACACAGATCACTGTTGGGGATGCTGGATGGCGGAGGACCTGGAGAGA 890
 QY 1456 GATGAAGCAAAACAGAGCGCTGAAGTCTATGATGAGACAAACTGCCACTGGAGGCTGC 1515
 Db 891 GAGGA---GAACCTGAGCTGAGTCTGTGTATGAGACAGACTGCCGTGGGATGGTTGC 947
 QY 1516 GCGAGGAGTTCGACACCCCAAGAGCAGCTTGTGACCACTATAAATAAGCAGCATATTTCAT 1575
 Db 948 AGCCAGGAGTTCGATTCCAGGAGCAGCTGTTGTCACACATCAACAGTGAGCATATCCAC 1007
 QY 1576 GGAGAGAAAGGAGTTCGTGTGAGGTGGCTGACTGCTCAAGAGACAGAAACCCCTTC 1635
 Db 1008 GGGGAGCGGAAGGAATCTGTGTCATTTGGGAGGTTCCTCCAGGAGCTGAGGCCCTTC 1067
 QY 1636 AAAGCCAGTATATGTTGATGTCATATGAGACACACACGCGGAGAGCCTCACAAA 1695
 Db 1068 AAGGCCATACATCTGTTGTCATATGCGCACACACGCGGAGAGCCACACAAAG 1127
 QY 1696 TGCACCTTTGAAGTTGCACAAAGCCCTACTCGAGACTAGAAAACCTTGAACACACCTTG 1755
 Db 1128 TGCACGTTTGAAGGCTTCGGAAGTCTTATTCACGCCCTTGAACCTCAAGACGACCTT 1187
 QY 1756 AGATCTCAGCTGGAGAGAACCATACGCTGTGTGAGCAGAGGTTGCAACAGGCTTTC 1815
 Db 1188 CGGTGCGCACACGGGTGAGAAGCTTACATGTGTGAGCAAGAAGGTTGCAAGAGGCTTTC 1247
 QY 1816 TCAATGCTCTGTATGCGGCCAAACACCAACAGACGACATTCACATGAGAAACCATAT 1875
 Db 1248 AGCATGCGAGTGACCGCCAGCCAGCCAGATCGGACCCCACTTCAATGAGAGCCATAC 1307
 QY 1876 GTGTCAAAATCCAGGCTGACTAAGGCTTACAGACCCCAAGCTCCCTCCGGAACAT 1935
 Db 1308 GTGTCAAGCTCCCGGCTGCACCAAGCGCTACACAGATCCAGCTCGCTCCGCAACAC 1367
 QY 1936 GTGAAGACAGTGTGCGCCAGAGCTCATGTCCACCAAGAGCAGCGAGGAGCATCC 1993
 Db 1368 GTGAAGACAGTGTGCTCCGAGTCCCGATCCACGCTGACCAAGCGCATCGAGGGGATGGCC 1425

RESULT 7

ID: 74625

AC AAF74625 standard; cDNA; 3326 BP.

AAE74625;

14-MAY-2001 (first entry)

Human GLI-1 nucleotide sequence SEQ ID NO:27.

SUFUH; GLI-1; Sonic hedgehog-patched signalling pathway; cancer;
 cell differentiation; tissue development; ss.

Homo sapiens.

W0200112655-A1.

22-FEB-2001.

14-AUG-2000; 2000WO-SE01576.

13-AUG-1999; 99SE-0002899.

(KARO-) KAROLINSKA INNOVATIONS AB.

Toftgard R;

XX

WPI; 2001-211199/21.

Novel peptides comprising fragments of two components of sonic
 hedgehog-patched signalling pathway, GLI-1 and SUFUH, useful for
 treating cancer and diseases influencing cell differentiation and
 tissue development

Example 3; Page 111-112; 115pp; English.

The present invention describes peptides consisting of fragments of GLI-1
 and SUFUH, respectively which are able to specifically bind to SUFUH and
 GLI-1, respectively. GLI-1 and SUFUH are components which interact in the
 sonic hedgehog (Shh)-patched (Pth) signalling pathway. The present
 invention also describes: (1) DNA sequences encoding the peptides; and
 (2) a monoclonal antibody or an antibody fragment directed against the
 peptides. The peptides have cytostatic activity, and can be used as
 Shh-Pth signalling pathway modulators. The peptides and monoclonal
 antibodies against them can be used for preparing a pharmaceutical
 composition for treating cancer. The peptides on contact with the GLI-1
 and SUFUH in vivo affects the Shh-Pth signalling pathway which is used
 in the treatment of cancer. The peptides comprising the peptide fragments
 of the signalling pathway are also useful for treating other diseases
 influencing cell differentiation and tissue development. The present
 sequence represents the human GLI-1 nucleotide sequence, which is used
 in an example from the present invention.

Sequence 3326 BP; 715 A; 1087 C; 879 G; 645 T; 0 other;

Query Match 6.5%; Score 329.4; DB 22; Length 3326;

Best Local Similarity 70.6%; Pred. No. 7.7e-64;

Matches 454; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 1372 GATGAAGACCTCCCGAGCGGCTCGGGGCGAGCAGCAAGCAGCCGGAAGCAAC 1431

Db 586 GAAGGTGATATGTCACGCCCACTCCACAGGATACAGGATCCCTGTGGGGATGCTG 645

QY 1432 CTTGTCAAGGAGGAGGGGACAAAGATGAAGCAAAACAGGAGCCTGAAGTCACTATGAG 1491

Db 646 GATGGCGGGAGGAGCCTCGAGAGAGAGGA---GAAGCGTGAGCCTGAATCTGTGTATGAA 702

QY 1492 ACAACATGCCACTGGGAGGCTCGCGGAGGAGTTCGACACCCCAAGAGCAGCTTGTGCAC 1551

Db 703 ACTGACTCGGCTGGGATGCTCGACCGAGGAATTTGACTCCCAAGAGCAGCTGGTGCAC 762

QY 1552 CATATAAATAACGACCATATTCATGGAGAGAAAGAGTTCGTGTGAGGTGGCTGGAC 1611

Db 763 CATATCAACAGGAGCAGCATCCAGGGGAGCGGAGGAGTTCGTGTGCCACTGGGGGGC 822

QY 1612 TGCTCAAGAGAGCAGAAACCCCTTCAAAGCCAGTATATGTTGGTAGTGCATATGAGAAGA 1671

Db 823 TGTCTCAGGAGCTGAGGCCCTTCAAAGCCAGTACATGCTGCTGCTTACATGCGCAGA 882

QY 1672 CACACGGCGAGAGCCTCAAAATGCATTTTGAAGTTGCAAAAGGCTACTACGAGA 1731

Db 883 CACACTGGCGAGAGCCACAAAGTGCACGTTTGAAGGTTGCGCGAAGTCACTACTCACGC 942

QY 1732 CTAGAAACTTTGAAACACACACTTGTAGATCTCACACTGGAGAGAAACCATACGCTGTGAG 1791

Db 943 CTGAAAACTCTGAAGACGACCTCGCGGTACACACGGGTGAGAGGCCATACATGTTGAG 1002

QY 1792 CAGGAAGTTGCAACAGGCTTTCTCAAAATGCCTCTGATCGGCCCAAAACACCAACAGAGA 1851

Db 1003 CACGAGGCTGCAGTAAAGCCTTCAGCAATGCCAGTGCACCGAGCCCAAGCAGCAAGATCGG 1062

QY 1852 AGCATTTCCAAATGAGAAACCATATGTGTGCAAAATCCAGGCTGCACACTAGCGTTACACA 1911

Db 1063 ACCCATTTCCAAATGAGAGCGGTATGTATGTAAAGTCCCTGCGTGCACCAACGCTATACA 1122

QY 1912 GACCAAGCTCCCTCGGAAACATGTGAACAGTGCATCGCGCCAGAGGCTCATGTGTCACC 1971

Db 1123 GATCCTAGCTCGCTGCGAANAACATGTCAAGACAGTGCATGCTGCTGACGCCCATGTGACC 1182

CC tumour formation. The antisense compounds are safely and effectively
 CC administered to humans. The present sequence represents human
 CC glioma-associated oncogene-1 DNA.

XX Sequence 3600 BP; 785 A; 1161 C; 949 G; 705 T; 0 other;

Query Match 6.5%; Score 329.4; DB 24; Length 3600;
 Best Local Similarity 70.6%; Pred. No. 7.9e-64;
 Matches 454; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 1372 GATGAAGACCTCCCGACGGGGCTGGGCGACAGACAGCCCGAAGAACACC 1431
 DB 664 GAAGGTATATGTCCAGCCCACTCCACAGCATACAGGATCCCTGGTGGATCTGT 723
 QY 1432 CTGTCAAGAGAGAGGAGGACAAAGATGAAGCAAGAGGCTGAGTATCATAGAG 1491
 DB 724 GATGGGGGGAGACCTCGAAGAGAGAGG---GAGCGTGGCTGATCTGTATGAA 780
 QY 1492 ACAAACTGCCACTGGGAGGAGGCTGGCGAGGAGTTGCACACCCAGAGAGCTTGTGCAC 1551
 DB 781 ACTGACTGCTGGATGGATGGCTGCAGCAGGAAATTTGACTCCCAAGAGCAGTGTGCAC 840
 QY 1552 CATATAATATACGACCATATTCATGAGAGAGAGAGAGTTGCTGAGGTGGCTGAC 1611
 DB 841 CACATCAACAGCGAGCATCTCACGGGAGGAGGAGTTCTGTCCACTGGGGGGGC 900
 QY 1612 TGCTCAAGAGAGAGAGAAACCTTCAGAGCCAGTATATGTTGTTAGTGCATATAGAGA 1671
 DB 901 TGCTCCAGGAGAGCTGAGGCGCTTCAGAGCCAGTACATGCTGTTGTTGATGCGAGA 960
 QY 1672 CACACGGGGAGAGAGCTCCACAAATGACCTTTGAGGTTGACACAAAGGCTTACTCGAGA 1731
 DB 961 CACACTGGCGAGAGACACACAGTGCACGTTTGAAGGGTGCAGAGTATATCTACGCC 1020
 QY 1732 CTAAATAACTGAAAACACACTTATCTACACTGAGAGAGAAACCATACGTGTGAG 1791
 DB 1021 CTGCAAAACCTGGAAGAGCGACCTCGGTTCACACGGGTGAGGAGCCATCATCTGTGAG 1800
 QY 1792 CACGAGGTTGCAACAGAGGCTTCTCAAAATGCTCTGATGCGCGCAACCAACAGAGA 1851
 DB 1081 CACGAGGCTGCTCAATTAAGCTTACAGATGCCAGTACAGCCAGCCAGCAATATCGG 1140
 QY 1852 ACGCATTCATGAGAAACCATATGTGCAAAATCCAGGCTGCTACATAGCCTTACACA 1911
 DB 1141 ACCCATTCATGAGAGAGCGGTATGTATGTATAGCTCCCTGGCTGCACAAACGCTATACA 1200
 QY 1912 GACCAAGCTCCCTCCGGAACATGTGAGAGAGTGCATGGCCGAGAGGCTCATGTACC 1971
 DB 1201 GATCCTAGCTGCTGCGAAGAAACATGTACAGACAGTGCATGTGCTGACGCCATGTGACC 1260
 QY 1972 AAGAAGCAGGAGGAGCATCATCTCGGCGCCGACAGCCCGGA 2014
 DB 1261 AAAGGCAACGCTGGGATGGCCCTGCTGCGGACACATCA 1303

RESULT 14
 ABO15578
 ID ABO15578 standard; DNA: 557 BP.
 XX
 AC ABO15578;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE oligonucleotide for detecting cytosine methylation SEQ ID NO 2169.
 XX
 KW Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200218632-A2.

XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP10074.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guelig D;
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + sequence listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridized to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridization to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridized to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 CC
 XX

Sequence 557 BP; 105 A; 52 C; 172 G; 228 T; 0 other;

Query Match 6.1%; Score 310.6; DB 24; Length 557;
 Best Local Similarity 72.4%; Pred. No. 6.7e-60;
 Matches 403; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 2984 GGAGGTGACGAGCGGGGAGCCACGCTACGCGGCGCCACCTGACCGCAGATG 3043
 DB 1 GGAGGTGTAGCGAGGGGAGTTACGTTACGGGGGCTTATTTGTGTGTACGATG 60
 QY 3044 CGCTGGGCGACGGCTGTAGAGAGGGCCAGCGACCCGGTGGAGAGGCTCGAGGGCTGG 3103
 DB 61 CGTGGGGTTACGGCTGTAGAGAGGGTATCGGTGGGATGATGTTGAGAGGTTGG 120
 QY 3104 CCTGCGCTGTGGCGGCTTACGAGCGCTGACGAGCTGCAACCCCGGGGATGGCCA 3163
 DB 121 TTTTGTGTTCTGTGTGCGCTTTTAGTAGTTTAGTATTTTTCGGGATGTGA 180
 QY 3164 CGTCCGCGAGAGCGCAGCTCTGCTTACAGATTACAGCGCGCCGAGGGCGGCACT 3223
 DB 181 CGTTGGCGGAGAGCGGTAGTTTGTGTTTAAATTAATACGGGCTTCGAGGGCGGTAGT 240
 QY 3224 CCGGAATCTCCACTGCTCCCTGCTGCTCCAGCATCACCGAAGACGTACCTTGAGT 3283
 DB 241 TTGGAATTTTAAATTCGTTTGTGTTTGTATTTATTCAGAAACGTTATTTTGAGT 300
 QY 3284 CCTGAGCATGAGCGGTGATGCAACCTGACAGATAGATTTCCGCGCGAGCAGCTGG 3343
 DB 301 TTTTGTATGACGCTTGATGTTAATTTGACAGATGAGATTTTGTGTGGACGACGTGG 360
 QY 3344 TGCAGTATTTAAATTCGAGAACAGAGGCTAGAGAGCAGCTCCCGACGCGCTCC 3403

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(without alignments)

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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	707	14.0	4960	US-09-907-843-3	Sequence 3, Appl
2	329.4	6.5	3600	US-09-657-042A-3	Sequence 3, Appl
3	90.8	1.8	3138	US-09-234-332-5	Sequence 5, Appl
4	83.2	1.6	2364	US-09-172-045-1	Sequence 1, Appl
5	68.6	1.4	7218	US-08-232-463-14	Sequence 14, Appl
6	61	1.2	7218	US-08-232-463-14	Sequence 14, Appl
7	55.4	1.1	8438	US-07-945-283-1	Sequence 1, Appl
8	51.8	1.0	4403765	US-09-103-840A-2	Sequence 1, Appl
9	50.4	1.0	1496	US-08-843-993-2	Sequence 2, Appl
10	50.4	1.0	1496	US-09-059-520A-2	Sequence 2, Appl
11	50.4	1.0	1496	US-09-334-275-2	Sequence 2, Appl
12	50.4	1.0	30001	US-08-125-468-1	Sequence 1, Appl
13	50.4	1.0	30001	US-08-474-933-1	Sequence 1, Appl
14	49.4	1.0	2744	US-09-071-101-1	Sequence 1, Appl
15	49.4	1.0	2744	US-09-369-618-1	Sequence 1, Appl
16	49.4	1.0	2744	US-09-369-618-1	Sequence 1, Appl
17	49	1.0	4695	US-08-231-193A-57	Sequence 1, Appl
18	49	1.0	4695	US-08-486-273A-57	Sequence 57, Appl
19	49	1.0	4695	US-08-940-086A-57	Sequence 57, Appl
20	49	1.0	4695	US-08-940-086A-57	Sequence 57, Appl
21	49	1.0	4695	US-08-935-105A-57	Sequence 57, Appl
22	49	1.0	4695	US-08-935-105A-57	Sequence 57, Appl
23	48.6	1.0	1147	US-08-761-277A-44	Sequence 44, Appl
24	47.6	0.9	1865	US-08-083-948-7	Sequence 7, Appl
25	47.6	0.9	1865	US-08-393-785-7	Sequence 7, Appl
26	47.6	0.9	1865	US-08-475-694-7	Sequence 7, Appl
27	47.6	0.9	1865	US-08-712-057-7	Sequence 7, Appl

C 28	47.6	0.9	2374	US-09-347-801-3	Sequence 3, Appl
C 29	47.6	0.9	2721	US-08-775-009-36	Sequence 36, Appl
C 30	47.6	0.9	3507	US-08-998-416-861	Sequence 861, Appl
C 31	46.8	0.9	614	US-09-178-109-3	Sequence 3, Appl
C 32	46.8	0.9	2064	US-09-142-791A-3	Sequence 3, Appl
C 33	46.8	0.9	2072	US-09-142-791A-3	Sequence 3, Appl
C 34	46.8	0.9	2104	US-09-142-791A-5	Sequence 5, Appl
C 35	46.8	0.9	2104	US-09-142-791A-5	Sequence 5, Appl
C 36	46.8	0.9	2121	US-09-178-109-1	Sequence 1, Appl
C 37	46.6	0.9	2353	US-08-922-06840-1	Sequence 1, Appl
C 38	46.4	0.9	43280	US-08-804-2270C-1	Sequence 1, Appl
C 39	46.2	0.9	1761	US-09-504-358-19	Sequence 19, Appl
C 40	46.2	0.9	1761	US-09-504-358-19	Sequence 19, Appl
C 41	46.2	0.9	2690	US-09-029-755C-1	Sequence 1, Appl
C 42	46.2	0.9	5117	US-08-854-585-1	Sequence 1, Appl
C 43	46.2	0.9	5117	US-08-854-585-1	Sequence 1, Appl
C 44	46.2	0.9	11471	US-09-504-358-16	Sequence 16, Appl
C 45	46.2	0.9	11471	US-09-504-358-16	Sequence 16, Appl

ALIGNMENTS

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RESULT 1
US-09-907-843-3
; Sequence 3, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
; CURRENT APPLICATION NUMBER: US/09/907.843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 4960
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (572)...(4348)
US-09-907-843-3

Query Match      14.0%; Score 707; DB 4; Length 4960;
Best Local Similarity 61.4%; Pred. No. 1.9e-156;
Matches 1441; Conservative 0; Mismatches 780; Indels 126; Gaps 14;

QY 1104 CTTCTCCGCGCCGCTCTCTCCACATGATGATGAGATGATGAGGAGCAACAGAGCTT 1163
      || || || || || || || || || || || || || || || || || || || || ||
DB 445 CTTCTCCGCGCCGCTCTCTCCACATGATGATGAGATGATGAGGAGCAACAGAGCTT 504

QY 1164 AGGTTCCGCTTTGGACAGCCCTTCATCCACCTGCGCCCACTTTTCCACACA 1223
      || || || || || || || || || || || || || || || || || || || || ||
DB 445 AGGTTCCGCTTTGGACAGCCCTTCATCCACCTGCGCCCACTTTTCCACACA 504

QY 1224 GAGGCTTATTCAGGAGATCTTACGCTTGAACCCCGTCAAGTCAAGTCAAGTCAAGT 1278
      || || || || || || || || || || || || || || || || || || || || ||
DB 565 GAGGCTTATTCAGGAGATCTTACGCTTGAACCCCGTCAAGTCAAGTCAAGTCAAGT 624

QY 1279 -----CCTTGTGAGTCTCTCCACAGAGCCGAGTGTGAGTGTGAGTGTGAGTGTG 1334
      || || || || || || || || || || || || || || || || || || || || ||
DB 625 CCTTGTGAGTCTCTCCACAGAGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 684

QY 1335 TGACCCGATGACACA---ACAGAGGTCCAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1391
      || || || || || || || || || || || || || || || || || || || || ||
DB 685 TGACCCGATGACACA---ACAGAGGTCCAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 744

QY 1392 AGGAGCTGAGGAGGAGCAAGCAAGCCCGAAGCAACCTTG-----1435
      || || || || || || || || || || || || || || || || || || || || ||
DB 745 AGGAGCTGAGGAGGAGCAAGCAAGCCCGAAGCAACCTTG-----1435

QY 1436 -----TCAAGAGGAGGAGGAGCAACCAAGATGAAG 1463
      || || || || || || || || || || || || || || || || || || || || ||

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Db	805	CTTCCCTCCCTCCCAAGGACGAGCTGGCTGACCTCAAGGAAGATCTGGACAGGGAGTGA	CTTCCCTCCCTCCCTCCCAAGGACGAGCTGGCTGACCTCAAGGAAGATCTGGACAGGGAGTGA	864
Oy	1464	CAAAACGAGACCTTA---AGTCATCTATGACACAAACTGCGACTGGGAAGGCTGGCCGAG	CAAAACGAGACCTTA---AGTCATCTATGACACAAACTGCGACTGGGAAGGCTGGCCGAG	1520
Db	865	TAAACGAGAGGCTGAGGTGGTGCATCTATGAGACCAACTGCACTGGGAAGACTGCACCA	TAAACGAGAGGCTGAGGTGGTGCATCTATGAGACCAACTGCACTGGGAAGACTGCACCA	924
Oy	1521	GGAGTTGCACACCCCAAGACGAGCTTGGGACCATATATAATGAACGACATATTCATGGAGA	GGAGTTGCACACCCCAAGACGAGCTTGGGACCATATATAATGAACGACATATTCATGGAGA	1580
Db	925	GGAGTAGACACACCCAGAGACGACGTGGTGGCATCTACATCAACACAGACACATCCACGGGA	GGAGTAGACACACCCAGAGACGACGTGGTGGCATCTACATCAACACAGACACATCCACGGGA	984
Oy	1551	GAAAGAAGAGTTGCTGTGCGAGGTGGCTGAGCTGCTCAAGAGACAGAAACCTTCAAGC	GAAAGAAGAGTTGCTGTGCGAGGTGGCTGAGCTGCTCAAGAGACAGAAACCTTCAAGC	1640
Db	985	GAAAGAAGAGTTGTTGTGTCGCGCTGGCGAGGCTCTACGCGGGAGCGAAGACCTTCAAGGC	GAAAGAAGAGTTGTTGTGTCGCGCTGGCGAGGCTCTACGCGGGAGCGAAGACCTTCAAGGC	1044
Oy	1641	CCAGATATGTTGGTAGTGATGACATGAAACACACAGGGCGAGAAAGCCATCAAAATGGAC	CCAGATATGTTGGTAGTGATGACATGAAACACACAGGGCGAGAAAGCCATCAAAATGGAC	1700
Db	1045	GCACTACATGCTGTGGTGGTGCATGCGGCGACACACGGGCGAGAAAGCCCAAGTGCAC	GCACTACATGCTGTGGTGGTGCATGCGGCGACACACGGGCGAGAAAGCCCAAGTGCAC	1104
Oy	1701	TTTTGAAGTTGTCACAAAGGCTTACTGAGACTAGAAACCTTGAAAAACACTTGAATC	TTTTGAAGTTGTCACAAAGGCTTACTGAGACTAGAAACCTTGAAAAACACTTGAATC	1760
Db	1105	GTTGAGAGGCTGCTCGAAGGCGTACTCCGCTGGAGAAACCTGAAACACACTCGCGTGC	GTTGAGAGGCTGCTCGAAGGCGTACTCCGCTGGAGAAACCTGAAACACACTCGCGTGC	1166
Oy	1781	TCACACCTGGAGAAACCATATACGTCTGTGAGCAGAAAGTTGACACAGGCTTTCTCAA	TCACACCTGGAGAAACCATATACGTCTGTGAGCAGAAAGTTGACACAGGCTTTCTCAA	1822
Db	1165	CCACACCGGGGAGAAAGCCATATGTGTGTGAGCAGAGGGGTGTGAACAAAGCCCTTCCAA	CCACACCGGGGAGAAAGCCATATGTGTGTGAGCAGAGGGGTGTGAACAAAGCCCTTCCAA	1224
Oy	1831	TGCCCTGTATGCGCCCAAAACACCAAAACAGACATTTCCATGAGAAACCATATGTGTG	TGCCCTGTATGCGCCCAAAACACCAAAACAGACATTTCCATGAGAAACCATATGTGTG	1880
Db	1225	CGCCTCGSAGCGGCGCAAGACACGAAATGCGACCACTCCCAAGGAAACCTTACTCTG	CGCCTCGSAGCGGCGCAAGACACGAAATGCGACCACTCCCAAGGAAACCTTACTCTG	1288
Oy	1881	CAAAATCCAGGCTGCACTAAGCTTATACACACACCAAGCTCCCTCCGGAACATGTGAA	CAAAATCCAGGCTGCACTAAGCTTATACACACACCAAGCTCCCTCCGGAACATGTGAA	1940
Db	1285	CAAGTCTCCAGCTGCACACAAAGATACACAGACCCAGCTCTCTCCGGAACATGTGAA	CAAGTCTCCAGCTGCACACAAAGATACACAGACCCAGCTCTCTCCGGAACATGTGAA	1344
Oy	1941	GACAGTGCATGGCCAGAGGCTCATGTGCACAGAAAGCAGCGGGGACATGCATCTGCG	GACAGTGCATGGCCAGAGGCTCATGTGCACAGAAAGCAGCGGGGACATGCATCTGCG	2000
Db	1345	AACGCTCCAGGCGCCCAATGCGCCACGTCAACCAAGAAAGCAGCGGATGAGCTGACTCGG	AACGCTCCAGGCGCCCAATGCGCCACGTCAACCAAGAAAGCAGCGGATGAGCTGACTCGG	1400
Oy	2001	GCGCCACACCCCGAGAGATTCGCGGACCACTTACAGTCCAGTGGCTGCGCCAGCCAG	GCGCCACACCCCGAGAGATTCGCGGACCACTTACAGTCCAGTGGCTGCGCCAGCCAG	2060
Db	1405	CACACCGCTGTCTAAAGATGGAGATGGGACATGAGGCGCGGACGAGACCTTGGCGGCC---	CACACCGCTGTCTAAAGATGGAGATGGGACATGAGGCGCGGACGAGACCTTGGCGGCC---	1461
Oy	2061	TCAGGAGACCTTGTGTGAGCAGAGACCTCACACACACTACTCTAAACGGGAAGATG	TCAGGAGACCTTGTGTGAGCAGAGACCTCACACACACTACTCTAAACGGGAAGATG	2120
Db	1482	-----AAGAGACACCGAGGCGAGCAGCAGCAGCAGGCGGTGAGAGCTG	-----AAGAGACACCGAGGCGAGCAGCAGCAGCAGGCGGTGAGAGCTG	1506
Oy	2121	CCTCCAGTGAAAACCGTCAAGGACAGAGAACCAATGACATCTCAGCCAAAGCCTGTGTGG	CCTCCAGTGAAAACCGTCAAGGACAGAGAACCAATGACATCTCAGCCAAAGCCTGTGTGG	2180
Db	1507	CCTGCAGCTCAGACCCATCAAGACCGAGAGCTCCGGGCTGTGTCATGCACGCCGGGGC	CCTGCAGCTCAGACCCATCAAGACCGAGAGCTCCGGGCTGTGTCATGCACGCCGGGGC	1566
Oy	2181	TCAGCTTCATGACGACGACCCAAAGTCCCCCATCAGCACTATTTCCA-----ACAGTGG	TCAGCTTCATGACGACGACCCAAAGTCCCCCATCAGCACTATTTCCA-----ACAGTGG	2234
Db	1557	CCAGTCGTCCTGACAGCAGCGAGGCCCTCTCTCTGTGGGAGTGGCCCCCAACATGACGTGG	CCAGTCGTCCTGACAGCAGCGAGGCCCTCTCTCTGTGGGAGTGGCCCCCAACATGACGTGG	1626
Oy	2235	GCTCGAGCTCTCTGTGACCGATGGAGGTAGATATAGAGACCTCAGTGGCCATGATGAAC	GCTCGAGCTCTCTGTGACCGATGGAGGTAGATATAGAGACCTCAGTGGCCATGATGAAC	2294
Db	1627	CGTGGAGATGCGCGGGGAGAGCGGGGCCCGGGACCTCGGGAGACGTATAGCGCACTGGATGACAC	CGTGGAGATGCGCGGGGAGAGCGGGGCCCGGGACCTCGGGAGACGTATAGCGCACTGGATGACAC	1688
Oy	2295	CCCAATTCATGAGACTCAACCATTTCC---ACTGCACACCAAGCCCTTGTCTTGCAAAGCAG	CCCAATTCATGAGACTCAACCATTTCC---ACTGCACACCAAGCCCTTGTCTTGCAAAGCAG	2351
Db	1687	ACCCCCAGGGGCGACACACTTAGCCCTGAGCTGCGCCCTCGCTGGTGGGCTCCAGCTGGG	ACCCCCAGGGGCGACACACTTAGCCCTGAGCTGCGCCCTCGCTGGTGGGCTCCAGCTGGG	1744
Oy	2352	GAGAAACCCCGGACAGGACCAAAATGATGAGAGCAGTAAAACTGTAAAGGCTTAAACAAGT	GAGAAACCCCGGACAGGACCAAAATGATGAGAGCAGTAAAACTGTAAAGGCTTAAACAAGT	2411
Db	1747	CAAAACATGTGACCAACCATGTGACCGGTTGAGCACTGTAAAGAGAGAGAACTAGTCACT	CAAAACATGTGACCAACCATGTGACCGGTTGAGCACTGTAAAGAGAGAGAACTAGTCACT	1806
Oy	2412	GAATGAAATGTTTCCGCGACTGAACCCCATTTACCCCTTAAAGCCCTGCGAGTCTTCC	GAATGAAATGTTTCCGCGACTGAACCCCATTTACCCCTTAAAGCCCTGCGAGTCTTCC	2471
Db	1807	CAAGGATTCCTGTCATGAGGGCGGGCGGACTTCCACACAGCGGAACACCAACTGCTTCC	CAAGGATTCCTGTCATGAGGGCGGGCGGACTTCCACACAGCGGAACACCAACTGCTTCC	1866
Oy	2472	TCTCATGGAATATGGCACACAGTCCAAACACACTCTGACGTTGGGTGGGGCCA-----	TCTCATGGAATATGGCACACAGTCCAAACACACTCTGACGTTGGGTGGGGCCA-----	2522

Db 1867 CTTCCCGGGAATGCTCCATCTTGAAACCTGATGTCAGTGGACGCGCGGCGCCG 1926
QY 2525 -----TGAGCGTCTTCCCGGAGAGAGGACTCTCTTGGGGTGAGCGTCACTATGCTGAA 2579
Db 1927 GGGGCTGTCTGGCGAAGCCGGCGGCTGTGTGGAGCTGTCCCGAGCGAGGTGAGCACTGTGAG 1986
QY 2580 CATGCTCAAC--AAGAGGAGACGAGCGCGCAGACACATACGTGAGCTCTACTGTAGACG 2636
Db 1987 CCAGGTGACGAGAGCGCGCGAGACGCTTCCACGACGAGCGGTCAAGTCTGGGCTCTACACGTGAG 2046
QY 2637 CCGCGGCTCTTACGGAATCTGAGCTTGTCTTCCAGCCGCGGCTCCAGCGAG--CGTC 2633
Db 2047 CCGCGGCTCTTCCGCAATCTCCCTACTTCTCCAGCGCGGCTCCAGCGAGGCGCTCGCC 2106
QY 2694 ACAGCGCGAGGAGCGCGCGCAGACAGTGAAGGTGAGCCACTGCTACAGACCCATCTCCAC 2753
Db 2107 CCTGGGCGCGCGCGCGCGCGCAGACAGCAAGTCTCCGCTACTCTACAGACCCCATCTCCAC 2166
QY 2754 CGAGCGCTTCGCGCGCTCCAGGAAAGCCAGCGAGCGGCTCGCCAGCTGTTCAG 2813
Db 2167 GAGACGCTGTGCGCGGCTCTGAGAGGAGCGCAGCGACAGCGGCGGCTCGGGCTGTCAA 2226
QY 2814 CCTCAGCGCGCGCGCGCAGAGTACCGGCTCAAGGCGCAAGTACCGGCTGTGCAAGAGGAGGCC 2873
Db 2227 CCTCAGCGCGGCGCAGCAATACGCTCTCGGCGCAAGTACGCGGAGCACTGTGGGCGCC 2286
QY 2874 GCGCGCGAGCGCCCTCGCCCAATCAGTGAAGAGTGAAGCGCCCTGAGCGCTGCT 2933
Db 2287 CCGCGCCACTCGCTGCGCGGCGCTGTGAGCGAGTGAAGCTGTGGAGACAGGCTGTGGCGTCT 2346
QY 2934 ---CGGGGATGCGCTTCAGAGCTGGGCGTGGCCCTGCTCTCAATTCATGCGCCGAGAGGTG 2990
Db 2347 GAGCGCGGCGGAGGAGCGCTGTGCGCGGCTGTGCGCCAGCCCACTGTGGGCGGCGGTGG 2406
QY 2991 CAGCGACGGGAGGAGCGCCAGCGCTAC-----GGCGGCGCGCACCTGTACCGCGACGA 3041
Db 2407 CAGCGACGGGCGCGACTTATGAGGCACAGGCGCGGCGGCTGTGGCGCTTCCCGCACGA 2466
QY 3042 TCGCGTGGGCGCACGGCGGTGAGGAGGAGGCCAGCCGCTGTGGAGACGCTCCGAGGGCT 3101
Db 2467 GCGCTCAGGCGGCGGAGACCGAGCGGCGCAGCGACCTGTGTGG--CGGCCGATGTGCT 2523
QY 3102 GCGCGCTGCTCTGTGAGCGCGCTTACAGAGCTCTGACAGCTGACACCCCGGAGTGGC 3161
Db 2524 GTCCCTGCGCGGGGTGACAGCGTTCACAGACACCCACAAGCTGAACCCCGGCGCGTGGC 2583
QY 3162 CAGCTCCGCGGAGAGCGCAGTCTGTGCTTACAGATTACACGCGGCGCGAGGGGCGCA 3221
Db 2584 GCGCTGTGCGCAGACGCGCAGGCGCTCGCGCTGAGCCACCGCAGCAGCGGCGCT 2643
QY 3222 GTCCGGAACCTTCCACTGTGTCCCTGTGCTCCCGCATCCGAGACGTCACCTGGA 3281
Db 2644 GCGCGCGCGCGCTTCTGCG--CCCGGCGCGCTTATGCACTACGCGAAGCGTGGCGATGA 2700
QY 3282 GTCCCTGACATGAGCGCTGATGCCAACCTGACAGTGAAGATTTCTTCCGCGAGACGT 3341
Db 2701 GCGCGGCGCGGAGAGTGAAGCGCGCGGCGCGGCGCGGCGCGGCGCGGAGGA 2760
QY 3342 GGTGCAAG 3348
Db 2761 CGACCTG 2767

RESULT 2
US-09-657-042A-3
; Sequence 3, Application US/09657042A
; Patent No. 6329203
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLOINMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTS-0148
; CURRENT APPLICATION NUMBER: US/09/657,042A


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Query Match      1.6%; Score 83.2; DB 4; Length 2364;
Best Local Similarity 51.5%; Pred. No. 4.4e-10;
Matches 271; Conservative 0; Mismatches 243; Indels 12; Gaps 3;

QY 1506 GGAAGGTCGCGGAGGAGTTCGACCCAGAGAGCTTGTGACCATATATAATACGA 1565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 845 GAAACCTGTGACAGACATTAGACAGATGATGACACTGTTACACATATGACAAATGCA 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1566 CCATATTCATG--AGAGAAAGAGAGTCTGTGCGAGTGTGAGTGTGCTCAAGGA 1622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 905 ACATATGGGGTCCAGAAACAAATATATCATATATGCTATGAGGAGATGTCGAGGG 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1623 GCAGAAACCTCTCAAGCCCATATATGTTGGTACTGATATGAAACACACGCGGGA 1682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 965 AGCTAATCTTTTAAAGCAATATATATGATGATATGATGATGATGATGATGATGATG 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1683 GAGGCTCAAAATGCACTTTTGAAGTTGACAAAGGCTTACTGAGACTAGAAACTT 1742
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1025 AAAACCTTTCATGCCCCCTCCCTGATGTTGGAAATCTTTCGACGCTTCAAGAAATCT 1084
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1743 GAAACACACTGAGATCTCACACTGAGAGAAACCATATGCTGTGAGCAGAGTTG 1802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1085 CAAGATCCACAAAGAACATCATAGGTGAGAGCATTCAGTGTGAGTTGAAGGCTG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1803 CAACAAGGCTTCTCAATGCTGATGCGCCCAACACACAAACAGACGATTCGAA 1862
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1145 CATATGAAGTTTGCACACAGAGGAGG---CAGGAAACAAACATATGATGATGATGATG 1201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1863 TGAGAAACCATATGTTGCAAAATCCAGGCTGACATTAAGCTTACACAGACCAAGCTC 1922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1202 ACATTAAGCATATATCTGCA--AGTGTGATATATATCTTACACTCACGCCAGCTC 1255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1923 CCTCGGAAACATGTAACAGACAGTGCAGGCCAGAGCTCATGTCACCAAGACAGG 1982
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1256 CCAAGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1983 AGGGGACATCATCTCGCGCCGACCCCGAGAGATTCCGCGCAGC 2028
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1316 CTCAGGGTACGATCTGCTACCCACACAGCATGTTTCTGCGCAGC 1361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:

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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15

US-08-232-463-14

Query Match      1.4%; Score 68.6; DB 1; Length 7218;
Best Local Similarity 5.0%; Pred. No. 1.8e-06;
Matches 20; Conservative 231; Mismatches 150; Indels 0; Gaps 0;

QY 372 GACGCTGTTCCATGAGACCCAGGAATGTTACATGAGACCCCACTACCACTCTCTCA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1052 GAGGAGCTGTCGATATATATATATATATATATATATATATATATATATATATAT 1111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 TCTTTCCTCCCTCCATCCATCCCTGATACCAATGATGCGAGCATGAGGCGGTTA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1112 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 492 CCATTAAGATCATCTCCGATCTCCATGATGATGATGATGATGATGATGATGATGATG 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1172 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 552 TACGATCCGAGCTGCCCTTATATAGATCTCCCAACACCGGAGCCGCTGCTCTTC 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1232 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 612 CGAGTCCCTCCAGCCCTCCATCCCTGATGATGATGATGATGATGATGATGATGATG 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1292 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 672 CTTCACAGCAGCCATCCCTCTCATGATCTGACAAACCGTGAGCGCTACAGCA 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1352 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 732 TGCGCCCATGACAGAGTACAGCCAGCAGAACTACTATATC 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1412 YYYYYYYYYYYYYYYYYYYYYYGTACCAATATCTCTATC 1452
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RESULT 6
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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RESULT 7
 US-07-945-283-1/c
 : Sequence 1, Application US/07945283
 : Patent No. 5352596
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Cheung Andrew K.
 : APPLICANT: Wesley, Ronald D.
 : TITLE OF INVENTION: Pseudotables Virus Deletion Mutants
 : TITLE OF INVENTION: Involving The EP0 and LTR Genes
 : NUMBER OF SEQUENCES: 7
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Curtis P. Ribando
 : STREET: 1815 No. 5352596th University Street
 : CITY: Peoria

QY	2604	CGCGAGCACCATTACAGCTCGGCGCTACTCCTGTAGCAGCGCCGCTCTCATGGAGATCTGCCCCG	26633
Db	6155	CCCCGGCGCACCCAGCAGCAGCAGCGG9TGCCGCGACGCGCGGACAGGGGGGGGGCCCG	60966
QY	2664	CTTCTCCAGCCCGCCCTCCAGCGAGGCGTCTACAGGCCAGGGCCGCGCGCGCAGAACGT9AG	27233
Db	6095	CTTCTCCAGCGCTCCCGCGCGCGCGGCGCGGCTCTCGGCGCGCCCGCGCGCGCGCGCCCT	60366
QY	2724	C -GTGGCCACACTCTACAGACCCCATCTCTACCGAGACGGCTCGCGCGCGTCCAGCGAGAGCC	27813
Db	6035	CGCGCGGAGGGGAGACCGCGGTCGTCAACCATTCACAGCAGCCGCGACGCGCTGTCTCGACGAGC	59766
QY	2782	AGCCAGAGCGAGCGCTGGCCAGCGCTGCTACAGCCCTACGCGCCGCGCAGAGTACCGCTC	28413
Db	5975	CGCGCGCGCGGAGGCGGATCTCTCGGCGCGCTTG9GCGCGGAGCCCGCTCTCTCA	59166
QY	2842	AAGGCCAAGTACGCGGCTGTGCACAGGAGGGCGCGCGCGAGCGCCCTCTGCCAATG9AG	29013
Db	5915	ACCCCACTCACTCTCAGTCTCCACCAAGCAGCTGGCGCTGACGCGCTGTGCGCGCGGCG	58566

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OY 2902 AGGATGAGCCTGAAGACGGCCCTGGGCTGCTCGGGGATCCCTCGAGCCTGGCGG 2961
    || || || || || || || || || || || || || || || || || || || || ||
DB 5855 CGGAGAGGACGAGGAGGAGCTGCGCTCGCGGGAGACGGGGGGGCGCCCTCGAGAGAC 5796
OY 2962 CTGCTTCACGTTTCATCCCGGAGAGGTGACGAGCGGGGAGCCACGAGCTTACGGGCG 3021
    || || || || || || || || || || || || || || || || || || || || ||
DB 5795 AGCGCCGGCGGGCGCGCGGAGAGAG--CGGCTTCGCGCGCGCGCGCTTCAGCAGC 5737
OY 3022 CGGCACCTCGACCGGACGATGCGCTGGGGCCACGCGGTAGAGAGGCCAGCAGCCGGT 3081
    || || || || || || || || || || || || || || || || || || || || ||
DB 5736 TCCAGAGGCGGGGCGACGACTGCGCTCCCGGGCGCTCGCCCTCGCCCGCGG 5677
OY 3082 CGGACAGCTCGGAGGGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3141
    || || || || || || || || || || || || || || || || || || || || ||
DB 5676 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCTGCTG 5617
OY 3142 TGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3172
    || || || || || || || || || || || || || || || || || || || || ||
DB 5616 TCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5586

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RESULT 8

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US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007 00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "a" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Query Match          1.0%; Score 51.8; DB 4; Length 4403765;
Best Local Similarity 46.0%; Pred. No. 0.21;
Matches 250; Conservative 0; Mismatches 287; Indels 6; Gaps 2;

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OY 2604 CGGCAGACCATATCAGCTGCGCTTACCTGAGCAGCCGCGCTCTCTAGGATTCGCCCTG 2663
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925653 CGGACACACCTGCCCCCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925594
OY 2664 CTTTCTCCAGCGCGCGCTCCAGGAGGCGTACAGAGCGCGCGCGCGCGCGCGCGCGCG 2723
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925593 CGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925534
OY 2724 CGTGGCGGACTCTTACGACCCCATCTCCACGCA--CGCCTCGCGCGCGCTCCAGCAAGC 2781
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925533 CGGTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925474
OY 2782 AGCCAGAGGAGCGGCTGCGCGAGCTGCTACAGCTCAGCGCGCGCGCGCGCGCGCGCG 2841
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925473 CGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925418
    || || || || || || || || || || || || || || || || || || || || ||
OY 2842 AAGGCGCAATAGCGCGCTCCACAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2901
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925417 AAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925358
OY 2902 AGGATGAGCCTGAAGACGGCGCTGCTGCGGGGATGCCCTGAGGCTTGGCGTGGCG 2961
    || || || || || || || || || || || || || || || || || || || || ||

```

```

DB 3925357 CGGCACACCGCGGAAACAGACCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925298
OY 2962 CTGCTTCACGTTTCATGCCCGGAGAGGTGACGAGCAGCGGGGAGCCACGAGCTTACGGGCG 3021
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925297 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925238
OY 3022 CGGCACCTCGACCGCGCGAGATGCGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 3081
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925237 GCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925178
OY 3082 CGGACAGGCTCCGAGGGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3141
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925177 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3925118
OY 3142 TGC 3144
    || || || || || || || || || || || || || || || || || || || || ||
DB 3925117 AGC 3925115

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RESULT 9

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US-08-843-993-2
; Sequence 2, Application US/08843993
; Patent No. 5739010
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Puri
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,993
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1496 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNOAT01
; CLONE: 727885
US-08-843-993-2

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Query Match          1.0%; Score 50.4; DB 1; Length 1496;
Best Local Similarity 57.7%; Pred. No. 0.018;
Matches 90; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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OY 1651 TTGTAAGCTATATGAGAGACACGCGGAGAGAGCTTACAAATGACTTTTGAAGT 1710
    || || || || || || || || || || || || || || || || || || || || ||
DB 877 TTGAAGAGCACAAGAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
OY 1711 TGCACAAAGGCTACTGAGACTGAAAGACTTGAAGACACTTGAATCTCAGACTGGA 1770

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Db 937 TGACATGGAAGTTGCTCGTCTGATGAGACTAACAAGACATTTCCGAAAACATACCTGCA 996
QY 1771 GAGAAACCATACCTGCTGTGAGCAGACGAGGTTGCAAC 1806
Db 997 ATCAACCTTTCAGTCCCGGACTGTGACCGCAGC 1032

RESULT 10

US-09-520A-2
Sequence 2, Application US/0905520A

Patent No. 6001971
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,520A
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0274 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1496 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNCOAT01
CLONE: 727885
US-09-520A-2

Query Match 1.0%; Score 50.4; DB 3; Length 1496;
Best Local Similarity 57.7%; Pred. No. 0.018;

Matches 90; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1651 TTGGTAGTCATATGAGACACACGCGGAGAGCCTTCAAAATGCACTTTGAAAGT 1710
Db 877 TTGAAAGCACACAGAGACACACAGAGAAAACCTTACAAATGTACATGGGAAGG 936
QY 1771 TGCAAAAGCCCTACTCGAGACATGAAAACCTGAAAACACACACTGTGATCTCACACTGGA 1770
Db 937 TGACATGGAAGTTGCTCGTCTGATGAGACTAACAAGACATTTCCGAAAACATACCTGGA 996
QY 1771 GAGAAACCATACCTGCTGTGAGCAGACGAGGTTGCAAC 1806
Db 997 ATCAACCTTTCAGTCCCGGACTGTGACCGCAGC 1032

RESULT 11

US-09-334-275-2

Sequence 2, Application US/09334275

Patent No. 6037132
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,275
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/059,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0274 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1496 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNCOAT01
CLONE: 727885
US-09-334-275-2

Query Match 1.0%; Score 50.4; DB 3; Length 1496;
Best Local Similarity 57.7%; Pred. No. 0.018;

Matches 90; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1651 TTGGTAGTCATATGAGACACACGCGGAGAGCCTTCAAAATGCACTTTGAAAGT 1710
Db 877 TTGAAAGCACACAGAGACACACAGAGAAAACCTTACAAATGTACATGGGAAGG 936
QY 1771 TGCAAAAGCCCTACTCGAGACATGAAAACCTGAAAACACACACTGTGATCTCACACTGGA 1770
Db 937 TGACATGGAAGTTGCTCGTCTGATGAGACTAACAAGACATTTCCGAAAACATACCTGGA 996
QY 1771 GAGAAACCATACCTGCTGTGAGCAGACGAGGTTGCAAC 1806
Db 997 ATCAACCTTTCAGTCCCGGACTGTGACCGCAGC 1032

RESULT 12

US-08-125-468-1
Sequence 1, Application US/08125468

Patent No. 5589385
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strath, Nancy
APPLICANT: Fantl, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07470
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/125,468
 FILING DATE: 22-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsevdos, Estelle J
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31,255-02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3241
 TELEFAX: (201)831-3305
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-125-468-1

Query Match 1.0%; Score 50.4; DB 1; Length 30001;
 Best Local Similarity 46.4%; Pred. No. 0.061;
 Matches 209; Conservative 0; Mismatches 231; Indels 10; Gaps 1;
 QY 2673 CCGCGCTCCAGCAGAGCGCTCAGAGCGCGCGCGCGCGAGCAAGTGAAGCGTGGCGGA 2732
 DB 8154 CCGCGCGCGCGAGAGCGCTCAGAGCGCGCGCGCGCGAGCGCGCGCGCGCGCGT 8213
 QY 2733 CTCCTACGAGCGCGCTCAGAGCGCGCGCGCGCTCCAGCAAGAGCGAGCGGA 2792
 DB 8214 CCAGCTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTCCAGCGAGCGTGGCGTGC 8273
 QY 2793 CGGC-----CTGCCAGCGCTGCTCAGCGCTCAGCGCGCGCGCGCGAGTACCGCTCA 2842
 DB 8274 GGGCGCAGATGAGAGCGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCGCATCGCA 8333
 QY 2843 AGGCCAAGTACGCGCGCTCCACAGAGAGCGCGCGCGCGCGCGCGCTGCCCAATGAGA 2902
 DB 8334 TGCCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGTCAAGGTCATCGCAT 8393
 QY 2903 GGATGAGCGCTGAGAGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 2962
 DB 8394 CGATCTCTGCTGCTGCTCAGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8453
 QY 2963 TGCTTCAGATTTCATGCCCGAGAGAGTGCAGCGAGCGCGCGCGCGCGCGCGCGCGCG 3022
 DB 8454 CCGCGCGCGCGCGAGCG 8513
 QY 3023 GCCACCTGACCG 3082
 DB 8514 GACTCGGCTGCG 8573
 QY 3083 GGACAGCGCTGCGAGCG 3112
 DB 8574 GGAGCGTGGCGCTGCG 8603

RESULT 13
 US-08-474-933-1
 ; Sequence 1, Application US/08474933
 ; Patent No. 5866410
 ; GENERAL INFORMATION:

APPLICANT: Ryan, Michael J.
 APPLICANT: Lotvin, Jason A.
 APPLICANT: Strahy, Nancy
 APPLICANT: Fantini, Susan E.
 TITLE OF INVENTION: Cloning of the biosynthetic pathway for
 TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosimids
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07470
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,933
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/125,468
 FILING DATE: 22-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsevdos, Estelle J
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31,255-02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3241
 TELEFAX: (201)831-3305
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-474-933-1

Query Match 1.0%; Score 50.4; DB 2; Length 30001;
 Best Local Similarity 46.4%; Pred. No. 0.061;
 Matches 209; Conservative 0; Mismatches 231; Indels 10; Gaps 1;
 QY 2673 CCGCGCTCCAGCAGAGCGCTCAGAGCGCGCGCGCGCGAGCAAGTGAAGCGTGGCGGA 2732
 DB 8154 CCGCGCGCGAGAGCGCTCAGAGCGCGCGCGCGCGAGCGCGCGCGCGCGCGT 8213
 QY 2733 CTCCTACGAGCGCGCTCAGAGCGCGCGCGCGCTCCAGCAAGAGCGAGCGGA 2792
 DB 8214 CCAGCTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTCCAGCGAGCGTGGCGTGC 8273
 QY 2793 CGGC-----CTGCCAGCGCTGCTCAGCGCTCAGCGCGCGCGCGCGAGTACCGCTCA 2842
 DB 8274 GGGCGCAGATGAGAGCGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCGCATCGCA 8333
 QY 2843 AGGCCAAGTACGCGCGCTCCACAGAGAGCGCGCGCGCGCGCGCGCGCTGCCCAATGAGA 2902
 DB 8334 TGCCTGCTGCG 8393
 QY 2903 GGATGAGCGCTGAGAGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 2962
 DB 8394 CGATCTCTGCTGCTGCTCAGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8453
 QY 2963 TGCTTCAGATTTCATGCCCGAGAGAGTGCAGCGAGCGCGCGCGCGCGCGCGCGCGCG 3022
 DB 8454 CCGCGCGCGCGCGAGCG 8513
 QY 3023 GCCACCTGACCG 3082

Db 8514 GACTGCGGTTGAGAGCGCCGACACCGCTCCACAGGGGATTGCAAGCGCGGGT 8573
 QY 3083 GGACAGGCTCCGAGGGGCTGGCCCTGCTC 3112
 Db 8574 GGAGCTGGCGCTCCCAACACGACGCG 8603

RESULT 14

US-09-071-101-1
 ; Sequence 1, Application US/09071101
 ; Patent No. 6013503
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, SI
 ; APPLICANT: Jaspers, Stephen R.
 ; TITLE OF INVENTION: HUMAN PROHORMONE CONVERTASE 4
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Zymogenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,101
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parker, Gary E.
 ; REGISTRATION NUMBER: 31,648
 ; REFERENCE/DOCKET NUMBER: 97-05
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6673
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2744 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 61...2325
 ; OTHER INFORMATION:
 ; US-09-071-101-1

Query Match 1.0%; Score 49.4; DB 3; Length 2744;
 Best Local Similarity 44.1%; Pred. No. 0.04;
 Matches 206; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 2582 TGTCTACAGAAAGGAGACAGAGCGCCGACATCAGCTGAGCTACCTAGGACGCGC 2641
 Db 908 TGACCAAGGGGCGCGGGGCTGGGACGCTCTTTCATCTGGGCTCGGCAAGCGGCGC 967
 QY 2642 GCTCTCAGGAGATCGCCCTGCTTTCACAGCGCGCTCCAGAGGCGCTCACAGCGC 2701
 Db 968 TGCACCTACGAACTGCACTGCGAGCGGTACACAAACAGCATTCACACGCTTTCGCTG 1027
 QY 2702 AGGGCGCGCGGAGAGAGTGAAGGTGGCCGACCTCTACGACCCCATCTCCACGAGGCT 2761
 Db 1028 GCACACACCTCCAGACAGAGCGCGGTGCTGGTACAGCAAGGCTGGGCTCCACCTCA 1087
 QY 2762 CGCGCCCTCCAGAGGAGCGACGCGAGCGAGCGGCTGCCAGCTGCTCAGCTCAGC 2821

Db 1088 CCACACCTACAGAGCGCGCTGGCCACCGACCCCAAGATGCTACCAAGAGCTGCATC 1147
 QY 2822 CCGCCAGCAGTACCGCTCAAGAGCCAGATACGCGGCTGCCACAGAGGCGCGCCGA 2881
 Db 1148 ACGGTGACAGACAGCAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207
 QY 2882 CGCCCTGCTCCAAACATGAGAGGATGAGCTGAAAGAGCGCTGCGCTGGCGGGATG 2941
 Db 1208 TGGCTTACGCTGAGAGGCGCAACCGCTTCTGCTGCTGAGACATGCAACCTGCTGG 1267
 QY 2942 CCGTCCGCTGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3001
 Db 1268 TCGCGCGCTTCAAGCGCGGCGACCTGCGAGCGCGGAGACTGAGAGCAACAGCGCG 1327
 QY 3002 GAGCCACGCTACAGGCGCGCGCCACCTGCGAGCGCGCAGCATGCGCTG 3048
 Db 1328 GCCAAGTACCATCTACTAGGATAGCGGCTGCTGAGCGCGCGCTG 1374

RESULT 15

US-09-369-618-1
 ; Sequence 1, Application US/09369618
 ; Patent No. 6100041
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, SI
 ; APPLICANT: Jaspers, Stephen R.
 ; TITLE OF INVENTION: HUMAN PROHORMONE CONVERTASE 4
 ; FILE REFERENCE: 97-05D2
 ; CURRENT APPLICATION NUMBER: US/09/369,618
 ; CURRENT FILING DATE: 1999-08-06
 ; EARLIER APPLICATION NUMBER: US 09/071,101
 ; EARLIER FILING DATE: 1998-05-01
 ; EARLIER APPLICATION NUMBER: US 60/044,015
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 2744
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (61)...(2325)
 ; US-09-369-618-1

Query Match 1.0%; Score 49.4; DB 3; Length 2744;
 Best Local Similarity 44.1%; Pred. No. 0.04;
 Matches 206; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 2582 TGTCTACAGAAAGGAGACAGAGCGCCGACATCAGCTGAGCTACCTAGGACGCGC 2641
 Db 908 TGACCAAGGGGCGCGGGGCTGGGACGCTCTTTCATCTGGGCTCGGCAAGCGGCGC 967
 QY 2642 GCTCTCAGGAGATCGCCCTGCTTTCACAGCGCGCTCCAGAGGCGCTCACAGGCGC 2701
 Db 968 TGCACCTACGAACTGCACTGCGAGCGGTACACAAACAGCATTCACACGCTTTCGCTG 1027
 QY 2702 AGGGCGCGCGGAGAGTGAAGGTGGCCGACCTCTACGACCCCATCTCCACGAGGCT 2761
 Db 1028 GCACACACCTCCAGACAGAGCGCGGTGCTGGTACAGCAAGGCTGGGCTCCACCTCA 1087
 QY 2762 CGCGCCCTCCAGAGGAGCGACGCGAGCGAGCGGCTGCCAGCTGCTCAGCTCAGC 2821
 Db 1088 CCACACCTACAGAGCGCGCTGGGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTG 1147
 QY 2822 CCGCCAGCAGTACCGCTTCAAGGCGCAAGTACGCGGCTGCCACAGAGGCGCGCGCG 2881
 Db 1148 ACGGTGACAGACAGCAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207
 QY 2882 CGCCCTGCTCCAAACATGAGAGGATGAGCTGAAAGAGCGCTGCGCTGCTGCGGATG 2941
 Db 1208 TGGCTTACGCTGAGAGGCGCAACCGCTTCTGCTGCTGAGAGGAGACATGCAACCTG 1267

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 19:51:21 ; Search time 8366 Seconds
(without alignments) 17584.829 Million cell updates/sec

Title: US-09-910-185-3

Perfect score: 5055
Sequence: 1 cgatactacgtggcatttt.....accctttttaaaaaaa 5055

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
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27: em_sts:*
28: em_un:*
29: em_vl:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. NO. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5055	100.0	5055	9	HUMGLI3A	M57609 Human DNA-b
2	4732	93.6	4743	10	HSAS0408	AI250408 Homo sapi
3	3696.6	73.1	5113	10	MMGLI3GEN	X85255 Mus musculus
4	2758.6	54.6	4962	5	AF231112	AF231112 Coturnix
5	2695.6	53.1	5025	5	AF231111	AF231111 Coturnix
6	2685.8	50.9	4632	5	AF222990	AF222990 Gallus ga
7	2557.6	41.9	18927	5	AC005028	AC005028 Homo sapi
8	2115.8	32.2	132169	2	AC026814	U42461 Xenopus lae
9	1625.2	32.2	175144	2	AC068502	AC026814 Mus muscu
10	1625.2	31.3	2175	5	AF303886	AC068502 Mus muscu
11	1581.4	29.8	186926	2	AC128489	AF303886 Gallus ga
12	1506.8	17.1	5849	10	MMGLI2	AC128489 Rattus no
13	864.8	15.8	4517	5	AF109923	X99104 M. musculus
14	796.2	15.6	4641	5	XU42462	AF109923 Xenopus l
15	789.2	15.2	2525	5	AF022818	U42462 Xenopus lae
16	770.8	15.0	6070	5	AF085746	AF022818 Gallus ga
17	756	14.9	3678	9	AB007296	AF085746 Danio rer
18	752.2	14.9	4909	9	AB007296	AB007296 Homo sapi
19	752.2	14.3	4156	5	AF348156	AB007296 Homo sapi
20	720.6	14.0	3729	9	AB007297	AF348156 Danio rer
21	707	14.0	4960	5	GGU60763	AB007297 Homo sapi
22	699	13.8	1889	5	AC096345	AB007297 Homo sapi
23	678.6	13.4	16964	2	AF316110	AC096345 Rattus no
24	610.2	12.1	855	5	AF316110	AF316110 Notophtha
25	541.6	10.7	2105	9	HUMTHP1	AF316110 Notophtha
26	541.6	10.7	2105	9	HUMTHP1	D14827 Human mRNA
27	496.4	8.5	186926	2	AC128489	D14827 Human mRNA
28	431.2	7.2	1934	5	GGU60762	AC128489 Rattus no
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30	360.2	6.6	3686	10	AB025922	U57454 Xenopus lae
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33	331.6	6.5	3587	9	BSGLI	AF026305 Mus muscu
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ALIGNMENTS

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DEFINITION Human DNA-binding protein (GLI3) mRNA, complete cds.
ACCESSION M57609.1
VERSION M57609.1 GI:183247
KEYWORDS SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
similarity

JOURNAL Mol. Cell. Biol. 10 (10), 5408-5415 (1990)
 MEDLINE 90377231
 PUBMED 2118997
 FEATURES
 SOURCE

Location/Qualifiers

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Query Match 100.0%; Score 5055; DB 9; Length 5055;
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RESULT 2

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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MEDLINE

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Copied from PCI US2003092 on 04-03-2004

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1 (bases 1 to 5113)
Thien,H., Buscher,D. and Ruther,U.
Cloning and sequence analysis of the murine Gli3 cDNA
Biochim. Biophys. Acta 1307 (3), 267-269 (1996)
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PUBMED
8688459
2 (bases 1 to 5113)
Thien,H.
Direct Submission
Submitted (15-JAN-1996) H. Thien, Medizinische Hochschule Hannover,
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Phasianinae; Coturnix.
REFERENCE 1 (bases 1 to 5025)
AUTHORS Borycki, A., Brown, A.M. and Emerson, C.P. Jr.
TITLE Shh and Wnt signaling pathways converge to control Gli gene
activation in avian somites
JOURNAL Development 127 (10), 2075-2087 (2000)
MEDLINE 20233829
PUBMED 10769232
REFERENCE 2 (bases 1 to 5025)
AUTHORS Borycki, A., Brown, A.M. and Emerson, C.P.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Cell and Developmental Biology, University
of Pennsylvania, 421 Curie Blvd, Philadelphia, PA 19104-6058, USA
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RESULT 6
AF222990
LOCUS      AF222990      4632 bp      mRNA      linear      VRT 03-MAR-2000
DEFINITION      Gallus gallus GLI3 mRNA, partial cds.
ACCESSION      AF222990
VERSION      AF222990.1 GI:7141287
KEYWORDS
SOURCE      Gallus gallus.
ORGANISM      Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 4632)
AUTHORS      Wang, B., Fallon, J.F., and Beachy, P.A.
TITLE      Hedgehog-regulated processing of Gli3 produces an
            anterior/posterior repressor gradient in the developing vertebrate
            limb
JOURNAL      Cell 100 (4), 423-434 (2000)
MEDLINE      20155426
PUBMED      10693759
REFERENCE      2 (bases 1 to 4632)
AUTHORS      Wang, B. and Beachy, P.A.
TITLE      Direct Submission
JOURNAL      Submitted (11-JAN-2000) Molecular Biology and Genetics, The Johns
            Hopkins University, School of Medicine, PCTB714, 725 N. Wolfe St.,
            Baltimore, MD 21205, USA

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                ALSSPTVSDLPFIRISPHRNPAAASPTSTPHYINPYMDYIRSLHSPSLMSLA
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[illegible]

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RESULT 8	
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LOCUS	6695 bp mRNA linear VRT 26-APR-1996
DEFINITION	Xenopus laevis neural specific DNA binding protein (Xgl113) mRNA, complete cds.
ACCESSION	U42461
VERSION	U42461.1
KEYWORDS	GI:1150835
SOURCE	Xenopus laevis.
ORGANISM	Xenopus laevis
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE	1 (bases 1 to 6695)
AUTHORS	Marine,J.-C., Bellefroid,E.J., Pendeville,H., Martial,J.A. and Pieler,T.
TITLE	An essential role for Xenopus G11-type zinc finger proteins in the early embryonic patterning of mesoderm and neuroectoderm
JOURNAL	Cell (1996) in press
REFERENCE	2 (bases 1 to 6695)
AUTHORS	Marine,J.-C., Bellefroid,E.J., Samain,H.P., Martial,J.A. and Pieler,T.

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Consensus quality: 128527 bases at least Q40
 Consensus quality: 129561 bases at least Q30
 Consensus quality: 130446 bases at least Q20
 Insert size: 126000; agarose-fp
 Insert size: 133000; pulse-field-gel
 Insert size: 132169; sum-of-contigs
 Quality coverage: 10.20x in Q20 bases; agarose-fp
 Quality coverage: 8.40x in Q20 bases; pulse-field-gel
 Quality coverage: 9.72x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

1
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 Matches 2025; Conservative 0; Mismatches 518; Indels 29; Gaps 6;

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Db 1741 CTCAGCAGCACTACCTCAAGGCGTGAAGATGCTTCCAAAGTGAAGCAGTCAAGTCAG 1800
QY 2149' AAGCCCAATGACATCTCAGCCAAAGCCCTGGTGTGCTCTTATGTCAGCAGCAGCAAGTCC 2208

Db 1801 AAACAATGACATCTCAGCAAGCCCTGGTGGTCAAGTCTACATGCGACGAGCAAGTCC 1860
QY 2209 CCCATCAGCAACTATTCCACAGTGGCTCGAGCTTCTCTGACCGGATGTAGTATA 2268
Db 1861 CCCATCAGCAACTATTCCACATGAGTGGATCGAGTCTGACTGTGGGCTAGTATA 1920
QY 2269 GGAGACCTCAGTGCCTCGATGAACCCCAATCATGACTCAACCACTTCCACTGCAAC 2328
Db 1921 GGAGACCTCAGTGTCTCATGATGAACCCCAATCATGACTTACCACTTCCACAGCCACC 1980
QY 2329 ACAGCCCTTGTCTTCAAGCCAGGAGAAACCCGCGAGGACCAATGATGGAGCAGTA 2388
Db 1981 ACAGCACTTGGCTTACAGGCGGAGGAAATATGACAGGACCAATGATGGAGCAAGTG 2040
QY 2389 AAACCTAGAAGGCTAAACCAAGTGAATGGAATGTTTCCGCGACTGAACCCCACTTCAACC 2448
Db 2041 AAATTAAGAAGTTGAACAAGTGAATGGAATGCTTCCAAGACTGAACCCGCTTCCACT 2100
QY 2449 CCTAAAGCCCTGCGGCTCTCTCTCATAGGAATGGCACACAGTCCCAACACACTGC 2508
Db 2101 TCCAAAGCCCGGACCTTTCGCGCTCTCATAGGAATGGTACCAATCAACAGCAGTGC 2160
QY 2509 AGCTTGGTGGGCC 2523
Db 2161 AGTGTAGGAGGATCC 2175
RESULT 12
AC128489/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-18L16, *** SEQUENCING IN PROGRESS
***, 78 unordered pieces.
AC128489
AC128489.1 GI:21909214
VERSION HTG: HTGS-PHASE1.
KEYWORDS Rattus norvegicus
SOURCE Rattus norvegicus
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 186926)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alzbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denny,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Haves,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Homs,J., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lousegh,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,

Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Vatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansley, J., Taylor, C., Taylor, T., Teifrod, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G., and Gibbs, R.
 Direct Submission
 Unpublished
 Reference 2 (bases 1 to 186926)
 Worley, K.C.
 Direct Submission
 Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GYTJ
 Center clone name: CH230-18L16
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 121757 bases at least Q40
 Consensus quality: 129238 bases at least Q30
 Consensus quality: 134548 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 78 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 1397: contig of 1396 bp in length
 * 1497: gap of unknown length
 * 2925: contig of 1428 bp in length
 * 3025: gap of unknown length
 * 4129: contig of 1105 bp in length
 * 4130: gap of unknown length
 * 4230: contig of 1377 bp in length
 * 5607: gap of unknown length
 * 5707: contig of 1090 bp in length
 * 6896: gap of unknown length
 * 6979: contig of 1039 bp in length
 * 7936: gap of unknown length
 * 8036: contig of 1397 bp in length
 * 9433: gap of unknown length
 * 9533: contig of 1267 bp in length
 * 10800: gap of unknown length
 * 10900: contig of 1313 bp in length
 * 12213: gap of unknown length
 * 12313: contig of 1010 bp in length
 * 13323: gap of unknown length
 * 13423: contig of 1057 bp in length
 * 13433: gap of unknown length
 * 14480: contig of 1393 bp in length
 * 14580: gap of unknown length
 * 15973: contig of 1405 bp in length
 * 16073: gap of unknown length
 * 17477: contig of 1405 bp in length
 * 17478: gap of unknown length
 * 17578: contig of 1083 bp in length
 * 18661: gap of unknown length
 * 18761: contig of 1029 bp in length
 * 19789: gap of unknown length
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 * 19889: contig of 1029 bp in length
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 * 19990: contig of 1029 bp in length
 * 20995: gap of unknown length
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 * 24493: contig of 1315 bp in length
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 * 27115: contig of 1811 bp in length
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 * 30086: gap of unknown length
 * 30186: contig of 1374 bp in length
 * 31560: gap of unknown length
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 * 35422: contig of 1262 bp in length
 * 36584: gap of unknown length
 * 36784: contig of 1628 bp in length
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 * 40560: gap of unknown length
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 * 42640: gap of unknown length
 * 42740: contig of 1780 bp in length
 * 44520: gap of unknown length
 * 44620: contig of 1340 bp in length
 * 45960: gap of unknown length
 * 46060: contig of 1154 bp in length
 * 47214: gap of unknown length
 * 47314: contig of 1549 bp in length
 * 48863: gap of unknown length
 * 48963: contig of 1819 bp in length
 * 50782: gap of unknown length
 * 50882: contig of 2227 bp in length
 * 53109: gap of unknown length
 * 53209: contig of 2493 bp in length
 * 55702: gap of unknown length
 * 55802: contig of 1364 bp in length
 * 57166: gap of unknown length
 * 57266: contig of 2135 bp in length
 * 59401: gap of unknown length
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 * 61478: gap of unknown length
 * 61578: contig of 1267 bp in length
 * 62845: gap of unknown length
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 * 64303: gap of unknown length
 * 64403: contig of 1569 bp in length
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 * 68143: contig of 1944 bp in length
 * 70087: gap of unknown length
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 * 74894: gap of unknown length
 * 74994: contig of 2234 bp in length
 * 77228: gap of unknown length
 * 77328: contig of 2033 bp in length
 * 79361: gap of unknown length
 * 79461: contig of 1598 bp in length
 * 81059: gap of unknown length
 * 81159: contig of 2358 bp in length
 * 83517: gap of unknown length
 * 83617: contig of 2040 bp in length
 * 85657: gap of unknown length
 * 85757: contig of 3334 bp in length
 * 89091: gap of unknown length

* 89092 89191: gap of unknown length
* 91185: contig of 1994 bp in length
* 91186: gap of unknown length
* 91285: contig of 2960 bp in length
* 94245: gap of unknown length
* 94246: contig of 2333 bp in length
* 94346: gap of unknown length
* 96678: contig of 3663 bp in length
* 96779: gap of unknown length
* 100441: contig of 1800 bp in length
* 100442: gap of unknown length
* 102341: contig of 1800 bp in length
* 102342: gap of unknown length

Query Match 29.8%; Score 1506.8; DB 2; Length 186926;
Best Local Similarity 78.9%; Pred. No. 9.1e-272;
Matches 1834; Conservative 0; Mismatches 482; Indels 8; Gaps 3;

QY 2515 GGTGGCCCATGACGCTTCTCCGGGACAGAGGACCTCTCTGGGTGACCTCACTATG 2574
Db 109501 GCGGGCCCGGGACCTTCTCCGGGACAGAGGATGATCTCTGGGTGATAGCTTCACTGTG 109442

QY 2575 CTGAACATGCTCAACAGAGGACAGCAGCGCAGCACCATCAGCTCGGCCCTACCTGAGC 2634
Db 109441 CTGAACAGCTCAACAGAGGACAGCAGCAGCACCATCAGCTCTGCCCTACCTGAGC 109382

QY 2635 AGCGCGCGCTCTCAGGGATCTCGCCCTGCTTCTCCAGCGCGCTTCCAGCGAGCGTCA 2694
Db 109381 AGCGCGAGATCTCTCGGGATCTCCCGCTGCTTTTCCAGCGAGGTCCTCAGTGAGGCATCG 109322

QY 2695 CAGCGCGAGGCGCGGACAGCTGACGGTGGCGGACCTCTCAGCACCCTATCTCCACC 2754
109321 CAGGCTGAAGGGGACCGCCAGAGTGTGAGTGTGGCGGACCTCTCAGATCCCTATCCACA 109262

2755 GAGCGCTCGCGCG - CTCACAGAGGACAGCAGCGGCGCTCCCGAGCTGCTCAG 2813
109261 GATGCTTCAGGAGTCTCAGCAGCGGACAGCGGAGTGTGCGTCCCGAGCTGCTCAG 109202

2814 CTTACGCGCGCGGACAGTACCGCTCAAGCGCAAGTACGCGGCTGCCAGAGGAGGCC 2873
109201 CTTACACCGCGTTCAGCAGTACCGCTCAAGCGCAAGTATGCTGCTGCCAGCGGTCGCC 109142

2874 GCGCGCGAGCGCGCTCCCAACATGAGAGGATGAGCCTGAAGACGCGCTGGCGCTGCT 2933
109141 GCACCCACACCTCTGCGCCACATGAGAAAGCTGAGCGCTGAAGACAGGATGGCGCTGCT 109082

2934 CGGGGATGCGCTCGAGCGCTGGCGCTGCTGCTCCAGTTCATGCCCCGAGAGGTGAG 2993
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2994 CGAGGGGAGCGCGGCTACGGGCGCGCGCACCTGACGCGCGAGATGCGCTGGGCGA 3053
109021 TGATGAGGAGGCGCATATACAGCAGGCGTCACTTACTGCTCATGATGCGCTAGCAA 108962

3054 CGCGTGAAGAGGCGCAGAGCGCGTGGGACAGGCTCCGAGGCGCTGGCGCTGCCCTG 3113
108961 CAGTGGAGAGAGCGGCGCGCTGTGAGGACCGTCTCGAGACATGCTCACTTCCCGAG 108902

3114 TGTGCGCGCTTCAGCAGCGCTCAGCAGCTGCAACCGCGCGGATGGCCACCTCCCGGGA 3173
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108721 GGATGCTGATGCTGATGCTGAATGATGAAGATTTCTGCGCAGATGATGTTGATGAT 108662

QY 3354 AATTCCTCAGAACAGAGGATGACAGCAGCTTCCCGAGCGCGCTCCCGGAGCAGAC 3413

Db 108661 GAAATTCACAGAACCAACAGAGGATGGCAGCAATTAACAGAGTTCCATCTCTGAAGATGG 108602
QY 3414 CAAAGTGGCCCGCAGCGCGCGGTGACTTTGACGCGCGCGCGGTGCGCAGACACCGAGCTGG 3473
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QY 3594 GCCCGCGCGCTGCGCGCAGACTCGCGCTTTGGTTCCTGCAACGCGCATGGTCTGCA 3653
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QY 3654 CCCGACAGAACCCCTTGA-----GGAGCGGCGCTCTGGGGCTATCAGACCTCTCGGGA 3707
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QY 3708 GAACAGAACCCCTACGCTGCGCGCAGAGCAGCTTGTATGCTCCACACAGCCCCGGGAAGTGG 3767
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QY 3888 CTCAAAGTGAAGAGACCCCGCATGCAAGGAGCGGGGCGGCGAGTGAATTTGGCGCTGCC 3947
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QY 3948 GGTAGCGCAATGAGTCACTGCGCAGCAGTGGTGAATGGCATGCAAGCAGGAGCCAGT 4007
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QY 4008 GGGCAGGGGTACCTGGCTCACCAGCTCTCGCGGACAGCAGTGCAGCAGCCCGGGGCGAG 4067
Db 108001 GGGCAGGGGTACATGCTCTCTCAGCTACTCAGTGGCAGCATGCAACACAGGGGCGCAG 107942

QY 4068 CGCGCGCGGTGAGCAGATGCTTGGCGAGATTTAGTGTACTTCAACATCAACATCTACCA 4127
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Ddb	107581		CTCATTTCCCTTCTCAGAGGCCAACTGCCTGCTCCAGGAGAATGGCTCTTGAAAAATTCTGA	107522	
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Ddb	107401	AATGTFCAGGGGCTTTGAGCCCCAGTAGTATTCAGAACCTTTCCCACAGCTCCCTCCGCTG	107342		
QY	4668	CACCACGCTCGGGGCTCCCTCCCAATCCAGTCCGCTGTCCTATGACGACCAACCAACATGG	4727		
Ddb	107341	CACCACGCTCGGGCATCCCTCCCATTCCT-TTCTGTCTCATGAGCACCAACCAACATGG	107283		
QY	4728	CPATCGGGACATGAGTTCTTTTGCTGACCTCCCTAGCGGAAGAAAATAAATCTCTTGCAG	4787		
Ddb	107282	CPATTTGGGATATGAGTTCTTTTGCTGACCTCCCTTGACAGTCCCTTGACAAGAAAGCAATGCTTGCGAG	107223		
QY	4788	TTATGCAATAGCTTTAGGAAAAAAAAAGACTCAACCAACGGRAA	4831		
Ddb	107222	TTATGCAATAGCTTTAGGAAAAAAAAAGACTCAACCAACGGRAA	107179		
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LOCUS					
DEFINITION			M.musculus mRNA for gli2 gene.		
ACCESSION	X99104				
VERSION	X99104.1 GI:1707589				
KEYWORDS	gli2 gene,				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Hughes,D.C., Allen,J., Morley,G., Sutherland,K., Ahmed,W., Prosser,J., Jettice,L., Allen,G., Mattel,M.G., Farrall,M. and Hill,R.E.				
TITLE	Cloning and sequencing of the mouse Gli2 gene: localization to the Dominant hemimelia critical region				
JOURNAL	Genomics 39 (2), 205-215 (1997)				
MEDLINE	97179222				
PUBMED	9027508				
REFERENCE	2 (bases 1 to 5849)				
AUTHORS	Hughes,D.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-JUL-1996) D.C. Hughes, University of Nottingham, MRC Institute of Hearing Research, University Park, Nottingham, Notts, NG7 2RD, UK				
FEATURES					
source	Location/Qualifiers 1..5849 /organism="Mus musculus" /strain="C57BL/6"				
gene	/db_xref="taxon:10090"				
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	<1..>5849 /gene="gli2"				
BASE COUNT	1334 a 1876 c 1524 g 1115 t				
ORIGIN					
Query Match	17.1%; Score 864.8; DB 10;				
Best Local Similarity	60.3%; Pred. No. 1.4e-151;				
Matches 1836; Conservative	0; Mismatches 1067; Indels 141; Gaps 19;				
QY	413	CCCACTACCAACCCCTCTCATCTTTTCCCTGCCCTCCATCCCTCTGTTACCAATTGATGCCA	472		
Ddb	237	CCCACGAGTTCCTCAGCAGCTCCTGCCGGCTTTCCACGCGCTTTGCCGATTGACATGA	296		

Db 1359 CCAACTGCCACTGGCAGAGTGCACCAAGGAGTATCACACAGGAGCAGCTGGTGCATC 1418
QY 1553 ATATAATACGACCATATTCATGGAGAGAGAGAGTTCGTGTGCAGGTGGCTGGACT 1612
Db 1419 ATATCAACAATGAACACATCCACGGGGAGAGAGAGTTCGTGTGCAGGTGGCTGG 1478
QY 1613 GCTCAAGAGAGAGAAACCCCTTCAAGCCAGCAGTATATGTTGGTAGTCATATGAGAAGAC 1672
Db 1479 GCACGAGAGAGAGAGCCCTTCAAGCCAGCAGTATATGTTGGTAGTCATATGAGAAGAC 1538
QY 1673 ACACGGGCGAGAGCCCTTCAAAATGACATTTTGAAGGTTGCACAAAGGCTTACTCGAGAC 1732
Db 1539 ACACGGGCGAGAGCCACACAAAGTGCAGCTTCAAGGCTTCAAGGCTTACTCTCGCC 1598
QY 1733 TAGAAAACCTTGAAGACACACTTCAGATCTCACACTGGAGAGAACATACGCTGTGTGAC 1792
Db 1599 TGAGAACCTTGAAGACACACTTCGTTTACACACAGAGAGAGGAGGATATGTTGTGAAC 1658
QY 1793 ACAGAGGTTGCAACAAAGGCTTTCTCAATGCTCTGATCGCGCCAAACACCAAAACAGAA 1852
Db 1659 ACAGAGGCTTGAACAAAGGCTTTCTCAATGCTCTGATCGCGCCAAACACCAAAACAGAA 1718
QY 1853 CGCATTTCAATGAGAAACCATATGTTGTGCAAAATCCAGGCTGCAGTAAAGCTTACACAG 1912
Db 1719 CTCACCTCCAATGAGAAACCCCTACATCTGCAAGATCCAGGCTGCACCAAGAGGTACACAG 1778
QY 1913 ACCCAAGCTCCCTCGGAAACATGTGAAGACAGTGCATGCGCCAGAGGCTCATGTGCACCA 1972
Db 1779 ACCCAAGCTCCCTCGGAAACATGTGAAGACAGTGCATGCGCCAGAGGCTCATGTGCACCA 1838
QY 1973 AGAAGCAGCGAGGAGACATCCATCTCGCGCCGACCCCGAGAGATTCGCGCAGCCCATTT 2032
Db 1839 AGAAGCAGCGAGGAGACATCCATCTCGCGCCGACCCCGAGAGATTCGCGCAGCCCATTT 1898
QY 2033 CACAGTCCAGGTCGCTGCGCCGACCATCTCAGGAGCCCTTGGTAGAGCAGGAGCTCA 2092
Db 1899 AGCCAGCGCGGAGCAGGAGTGCC-----GGGACCTGAGGAGAGTGTGGAGGCCA 1949
QY 2093 GCAACACTACCTCAAGCGGAGAGATGCTCCAGGTGAAACCGTCAAGGCGAGAGAGC 2152
Db 1950 GTAGCAGCAGCCACATCTGGAGGAGTGCATATCAATCAAGCCATCAAGCAGAGAGCT 2009
QY 2153 CAATGACATCTCAGCAAGCCCTGGTGTGCTTCATGACGAGCCCAACAGTCCGCCCA 2212
Db 2010 CCGGGCTTTGTAGTCAGTCCAGCCCGGGGCCAGTCACTCTGACGAGCGAGCCCTCTCCCC 2069
QY 2213 TCAGCAACTATTCCA-----ACAGTGGGCTCGAGCTTCTCTGACGATGGAGTAGTA 2266
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QY 2267 TAGGAGACCTCAGTGCATCGATGAAAC-----CCCAATCATGGACTCAACCATTTCCACTG 2323
Db 2130 TGGGAGACCTGACAGCAGTGGCTGACAGCTGTCAGGAGCTGACACCTCAGCCCTGGGTG 2189
QY 2324 CAACACAGCCCTTGTGTTGCAAGCAGGAGAAACCCCGCAGGGACCAAAATGGATGGAGC 2383
Db 2190 CACCTTCCACTGCTGGCTTCAGCTGCGCAACACATGAGCAGCCGTGCATCGCTTTGAGC 2249
QY 2384 ACGTAAACTAGAAAGGCTTAAACAGAGTGAATGGATGTTTCCCGCAGCTGAACCCCATTC 2443
Db 2250 AGCTGAAGAGAGAGAGCTCAAGTCACTGAAGGATTCCTGCTGCTGGGCGGCCAGCTC 2309
QY 2444 TACCCCTTAAAGCCCTGCGGTCTCTCTCTCATAGGAAATGG-----CACACAGTCCA 2497
Db 2310 CACACACCGCCACACCAAGCTGCTCCCTTCCAGTCAATGGTCTGCTCGGAAACT 2369
QY 2498 ACAACACTGCGAGTGGTGGGCCCATGAGCCTTCTCCCGGCGAGAAAGCGACCTCTCTG 2557
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QY 2789 GCGAGGCGCTGCCAGCCTGCTCAGCCTCAGCGCCGCGCCAGCAGTACGCGCTCAAGGCCA 2848
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RESULT 14

AF109923

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

AF109923 4517 bp mRNA linear VRT 29-APR-1999
Xenopus laevis zinc finger protein Gl12 (Gl12) mRNA, complete cds.

AF109923.1 GI:4704616

Xenopus laevis.

Xenopus laevis.

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Xenopodinae; Xenopus.

1 (bases 1 to 4517)

Lee, J., Platt, K.A., Censullo, P. and Ruiz i Altaba, A.

Gl12 is a target of Sonic hedgehog that induces ventral neural tube

development 124 (13), 2537-2552 (1997)

9735996

9216996
 2 (bases 1 to 4517)
 Brewster, R., Lee, J. and Ruiz i Altaba, A.
 Gli2/zic factors pattern the neural plate by defining domains of
 cell differentiation
 Nature 393 (6685), 579-583 (1998)
 MEDLINE
 9634234
 3 (bases 1 to 4517)
 Brewster, R. and Ruiz i Altaba, A.
 Direct Submission
 Submitted (28-NOV-1998) Cell Biology, Skirball Institute, NYU
 Medical Center, 540 First Avenue, New York, NY 10016, USA
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 BASE COUNT 1295 a 1292 c 990 g 940 t
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 Best Local Similarity 58.2%; Pred. No. 9.5e-139;
 Matches 1761; Conservative 0; Mismatches 1128; Indels 138; Gaps 15;
 QY 428 CTCATCTTTTCCCTCCCTCCCTCCCTGTATACCAATTGATGCGACATGAGGGCC 487
 DB 81 CTCCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 140
 QY 488 GTTACCATTCAGATTCATCCGATTCCTCCATTCGATGATGACTTCGCGCTTATCTAGTA 547
 DB 141 GATACCATTCAGATTCATCCGATTCCTCCATTCGATGATGACTTCGCGCTTATCTAGTA 200
 QY 548 GCCTTACGATTCGGAGCTCCCTTCATTCAGGATTCCTCCACACACACACACACAC 607
 DB 201 GCCTTACGATTCAGATTCCTCTTAATACGCTCTCCCTCTCCCTCTCCCTCTCCCT 260
 QY 608 CTTCCGAGTCTCCCTTCAGCCCTCCACATCCCTACATTAATCCCTACATGAGTATATCC 667
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QY	428	CTCATCTTTTCCGTGCCTTCCATCTCCTGTACCATTGATGCCACACATCATGAGGGCC	487		
Db	78	CTCCTCTCTCCGTGCCTTCCACCCCTCCCTCTCCCATTTGAAATGCGCCCAACAGAGGAA	137		
QY	488	GTATACATTACGATCCATCTCGGATTTCCCTCATTTGCATATGACTTTCGGCTTATCTAGTA	547		
Db	138	GATACCAATTATGACACACATAGGCAATTCACACTCTCCATGGCCCCCGACTCTCAGTGGCA	197		
QY	548	GGCCTACGTTATCGGAGACCTTCGCTTCATTAGGATCTCCCCACACCCGGAACCCGCTGCTG	607		
Db	198	GGCCTGTGATTTACAGACATTTCTTTAATCGGCTCTCCCCACACTCTCTGGGTACAACAG	257		
QY	608	CTTCCGAGTCTCCCTTCAGCCCTCCACATCCCTCATTAATCCCTACATGGACTATATCC	667		
Db	258	AGTTTGGTCATGCCATCATATTATGTAGCCCCACATGGAGCATTAACCTG-----C	308		
QY	668	GCTCCTTGACAGCAGCCCCATCGCTCTCCATGATCTCAGCAACCCCTGGGCTGAGCCCTA	727		
Db	309	GTCTGTGACACAGACCCCAACCTGTCTATGATCTCTGAGCCCTGTGTCTCAGCCCAAG	368		
QY	728	CAGATCGCGCCCATG-----	742		
Db	369	CAGAAGTTGCCCATGAGCACTTAAAGAAGGGGTATCTATGGTTTAGCACTCCCGCGC	428		
QY	743	---CAGGAGTACGCCACAGAGAATACTATCATCAGATGGCCCTGCTAACTGGCCACGCGCA	799		

Copied from PCIUS2003092 on 04-03-2004

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/notes="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT      202 a 253 c 258 g 157 t 1 others
ORIGIN

Query Match      16.3%; Score 826; DB 14; Length 871;
Best Local Similarity 97.9%; Pred. No. 8.4e-179;
Matches 847; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

QY 3789 TGAACAGCCCTGTAAAGCCCGCCAGTATGGGAACCTCTCAACAGCGCAGCCAGTGGCCCC 3848
Db      |||||||
QY 3849 TGGTGCACTCGACGGTGCCTGTGTGCCGGGATTCAGAGCCTCAAGCTCAAGAGCACCCC 3908
Db      |||||||
QY 3909 CATGCAAGGAGCGGGGGCCAGCTGAATTCGGCCTGCCGTAGCGCCCAATAGTACAGC 3968
Db      |||||||
QY 121 CATGCAAGGAGCGGGGGCCAGCTGAATTCGGCCTGCCGTAGCGCCCAATAGTACAGC 180
QY 3969 TGGCAGCATGCTCAATGGCATCGACAGCAGACAGCCAGTGGACAGGGGTACCTGGCTCA 4028
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QY 181 TGGCAGCATGCTCAATGGCATCGACAGCAGACAGCCAGTGGACAGGGGTACCTGGCTCA 240
QY 4029 CCAGCTCTCTCGGCGACAGCATCGACACCCCGGGGCGAGCCCGCCCGGTTCAGCAGATGCT 4088
Db      |||||||
QY 241 CCAGCTCTCTCGGCGACAGCATCGACACCCCGGGGCGAGCCCGCCCGGTTCAGCAGATGCT 300
QY 4089 TGGCGCAGATTAGTGCTACATCAACATCAACATCAACATCAACATCAACATCAACATCAAC 4148
Db      |||||||
QY 301 TGGCGCAGATTAGTGCTACATCAACATCAACATCAACATCAACATCAACATCAACATCAAC 360
QY 4149 AGGGGCTCAGCGATGGGCGAGCGCCGTCAGCTTGGCAGTGTGTCAGGGGTACCGACCC 4208
Db      |||||||
QY 361 AGGGGCTCAGCGATGGGCGAGCGCCGTCAGCTTGGCAGTGTGTCAGGGGTACCGACCC 420
QY 4209 ATGTGCGAGCTTTGGGGCGAGCGCGCGAGCGCTATGCGAGGGGACAGCCTTGCTCTGCA 4268
Db      |||||||
QY 4269 GTGAGAGAGCTCAGTGACACAGTCAAGCTGACAGCTGACAGGTGAATGTATCAAGATGGAGAT 4328
Db      |||||||
QY 4329 GAAAGGCGAGCCCGCTGCTCTAATCTGAGAACTACTCTGCTGCTGCTGCTGCTGCTGCTGCT 4388
Db      |||||||
QY 541 GAAAGGCGAGCCCGCTGCTCTAATCTGAGAACTACTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 4389 CCAAAACCGTGGGCTTCAGTGACAGACAGCAAGCTGGTTCATCTCTATTTTCAGAGCGC 4448
Db      |||||||
QY 601 CCNAAACCGTGGGCTTCAGTGACAGACAGCAAGCTGGTTCATCTCTATTTTCAGAGCGC 660
QY 4449 CAGCTGCTGCTACAGGGGACAGCGCCCAAAACCTCTGAGTTACTTTTCCCGAGGTGCTAA 4508
Db      |||||||
QY 661 CAGCTGCTGCTACAGGGGACAGCGCCCAAAACCTCTGAGTTACTTTTCCCGAGGTGCTAA 720
QY 4509 TCAGGTGACAGCAGTGGACAGCTCGACAGCCATGACCTGGAGAGGGGTACAGATTGA 4568
Db      |||||||
QY 721 TCAGGTGACAGCAGTGGACAGCTCGACAGCCATGACCTGGAGAGGGGTACAGATTGA 780
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BASE COUNT      239 a 278 c 278 g 203 t
ORIGIN

Query Match      15.4%; Score 778; DB 13; Length 998;
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QY 4018 TACCTGCTCAGCAGCTCTCTCGGCGAGCATGCGAGCAGCCCGGGGAGCGCCCGCGT 4077
Db      |||||||
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QY 4078 CAGCAGATGCTTGGGCGAGATTAGTGCTACCTCACACATCAACATCTACCAAGGCGCAGAG 4137
Db      |||||||
QY 121 CAGCAGATGCTTGGGCGAGATTAGTGCTACCTCACACATCAACATCTACCAAGGCGCAGAG 180
QY 4138 AGCTGCTGCCAGGGGCTCAGCGCATGGGCGAGCCGCGCTCAAGCTTGGCAGTTGTCAGG 4197
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Db 181 AGCTGCTGCGAGGGGCTACGGCATGGGCGAGCGCTCAAGCTTGCGAGTTGTCAGG 240
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 Db 301 CTTGCTCTGAGTCAGCAGCAGCTGAGTACACAAAGTCAGACCTGCGAGGGTGAATGATC 360
 QY 4318 AAGATGAGATGAAGAGCGAGCCCATCGCTGTGCTTAATCTGAGAAATGATCTGTT 4377
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 QY 4558 GTACAGATTGACTTCGATGCCATCATAGACGATGGGACCACTCCAGCCTGATGTCGGG 4617
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 Db 721 CGGGCGCTCCCTCCATTCCTCCAGTCCGCTGCTGATGACCAACCAATGCTATGCGGG 779
 QY 4737 ACATGAGTTCTTTCGTCGACC--TCCCTAGCGGAAGAAAGCAATTC--TTGCGATTATG 4792
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ACCESSION AA889686
 VERSION AA889686.1 GI:3016565
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 890)

REFERENCE

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaplib-femail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
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 was prepared from mRNA obtained from Clontech Laboratories
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 TGTTCACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
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 went through one round of normalization to Cots5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 224 a 196 c 219 g 248 t 3 others
 ORIGIN

Query Match 14.1%; Score 714.6; DB 9; Length 890;
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Db 298 AACCAACGAAATCAATAGAGTTGAAGAGATTAAACTGACTTTTGGCTGTTTTT 239
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VERSION AUI23517.1 GI:10948233
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 763)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Ishigai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
Y., Sugano,S., Ishigai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Query Match 13.7%; Score 692.2; DB 9; Length 763;
Best Local Similarity 98.2%; Pred. No. 4.5e-148;
Matches 709; Conservative 0; Mismatches 11; Indels 2; Gaps 1;
QY 3199 TACACGCGCCCGAGGGGGCCAGTCCCGAATTCGACTGTCCTCCCTGTCTCCCGAGC 3258
Db 1 TACACGCGCCCGAGGGGGCCAGTCCCGAATTCGACTGTCCTCCCTGTCTCCCGAGC 60
QY 3259 ATCACCGAAGCTCACCTGGAGTCCCTGACATGGAGCTGATGCCAACCTGAACGAT 3318
Db 61 ATCACCGAAGCTCACCTGGAGTCCCTGACATGGAGCTGATGCCAACCTGAACGAT 120
QY 3319 GAGGATTTCTCCGCGAGACGCTGTGTGAGTATTAAATTTCCAGAACCAAGAGGTAC 3378

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Db 121 GAGGATTTCTGCGGAGCAGCTGTGTGAGTATTAAATTTCCAGAACCAAGAGGTAC 180
QY 3379 GAGCAGACATTTCCCGAGCGGCTCCCGGAGCAGCAAGATGCCCCACGGCCGGTGCAC 3438
Db 181 GAGCAGACATTTCCCGAGCGGCTCCCGGAGCAGCAAGATGCCCCACGGCCGGTGCAC 240
QY 3439 TTTTACGCGCGCGGCTGCGCAGCAGCAGCAGCTGCGCCAGCAGTTTCCATGCCCTCGAGCAG 3498
Db 241 TTTTACGCGCGCGGCTGCGCAGCAGCAGCAGCTGCGCCAGCAGTTTCCATGCCCTCGAGCAG 300
QY 3499 CCCTGCCCCGAGGCGCAGCAAAACCGACTGCCCATTCAGTGGAAACGAGTCAAGTCCGGGA 3558
Db 301 CCCTGCCCCGAGGCGCAGCAAAACCGACTGCCCATTCAGTGGAAACGAGTCAAGTCCGGGA 360
QY 3559 AGCGCCGACCTGTCTCTCAAGCTCAAGTGTGGGCGCGGCGGCTGTGCGCGCAGACT 3618
Db 361 AGCGCCGACCTGTCTCTCAAGCTCAAGTGTGGGCGCGGCGGCTGTGCGCGCAGACT 420
QY 3619 CGCGCTTTTGGGTTCTCAACGGCATGTCTCCACCGCAGAACCCCTTGAGGAGCGGG 3678
Db 421 CGCGCTTTTGGGTTCTCAACGGCATGTCTCCACCGCAGAACCCCTTGAGGAGCGGG 480
QY 3679 CCTGCTGCGGGCTATCAGACCCCTCGGGGAGAACAGCAACCCCTACGSGTGGCCCGCAGACAC 3738
Db 481 CCTGCTGCGGGCTATCAGACCCCTCGGGGAGAACAGCAACCCCTACGSGTGGCCCGCAGACAC 540
QY 3739 TTGATGCTCCACACACAGCCCCGGGAGTGGCCACAGTGGAAACGCTTCCATGAACAGCCC 3798
Db 541 TTGATGCTCCACACACAGCCCCGGGAGTGGCCACAGTGGAAACGCTTCCATGAACAGCCC 600
QY 3799 TGTAAAGCCCGCAGTAGTGTGGAAGTCTCAACAGGAGCAGTGGCCCTGTGTGCACTC 3858
Db 601 TGTAAAGCCCGCAGTAGTGTGGAAGTCTCAACAGGAGCAGTGGCCCTGTGTGCACTC 660
QY 3859 GACGGTGCCTGTGTGCGCGGAGTTCAA--GCCTCAAAGCTGAAGAGACACCCCATGCAAG 3916
Db 661 GACGGTGCCTGTGTGCGCGGAGTTCAAAGGCTCAAAGAGCTGAAGAGACACCCCATGCAAG 720
QY 3917 GG 3918
Db 721 GG 722

RESULT 5
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LOCUS 603072918F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164757 5',
DEFINITION mRNA sequence.
ACCESSION BI830216
VERSION BI830216.1 GI:15941766
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 702)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1409 row: d column: 06
High quality sequence stop: 695.
FEATURES
Location/Qualifiers
1..702
source

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/organism="Homo sapiens"
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 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 site: 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

BASE COUNT 143 a 242 c 218 g 99 t

Query Match 13.6%; Score 688.4; DB 13; Length 702;
 Best Local Similarity 99.7%; Pred. No. 3.3e-147;
 Matches 700; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3374 GGTACGACGACGACTTCCCGAGCGCCCTCCCGGACGACGACAAAGTGCCTCCCGAGCGCGG 3433
 Db 1 GGTACGACGACGACTTCCCGAGCGCCCTCCCGGACGACGACAAAGTGCCTCCCGAGCGCGG 60
 QY 3434 GT-GACTTTGACGCGCGCGGCTGCAGACAGCCAGCTGGCGAGAGTTCCATGCCCTC 3492
 Db 61 GTGGACTTTGACGCGCGCGGCTGCAGACAGCCAGCTGGCGAGAGTTCCATGCCCTC 120
 QY 3493 GAGCAGCCCTGCCCGGAGGCGACGACAAACCGACCTCCCATTCAGTGGAAACGAGTCAGC 3552
 Db 121 GAGCAGCCCTGCCCGGAGGCGACGACAAACCGACCTCCCATTCAGTGGAAACGAGTCAGC 180
 QY 3553 TCCGGAAGCGCGACCTGTCTCTCTCCAAAGCTCAAGTGTGGCGCGCGCGCTGTGGCG 3612
 Db 181 TCCGGAAGCGCGACCTGTCTCTCTCCAAAGCTCAAGTGTGGCGCGCGCGCTGTGGCG 240
 QY 3613 CAGACTCGGCGCTTTGGTGTCTGCACGCGATGGTGTCTCACCGCGAGAACCCCTTTGAGG 3672
 Db 241 CAGACTCGGCGCTTTGGTGTCTGCACGCGATGGTGTCTCACCGCGAGAACCCCTTTGAGG 300
 QY 3673 AGCGGGCTCTGCTGGGCTATCAGACCCCTCGGGGAGAACGACCAACCCCTACGGTGGCCCA 3732
 Db 301 AGCGGGCTCTGCTGGGCTATCAGACCCCTCGGGGAGAACGACCAACCCCTACGGTGGCCCA 360
 QY 3733 GAGCAGTTGATGCTCCACACAGCCCGGAGAGTGGCACCAAGTGGAAACGCCCTTCCATGAA 3792
 Db 361 GAGCAGTTGATGCTCCACACAGCCCGGAGAGTGGCACCAAGTGGAAACGCCCTTCCATGAA 420
 QY 3793 CAGCCCTGTAAAGCCCGGAGTATGGAACTGTCTCAACAGGCGAGCCAGTGGCCCTGTGT 3852
 Db 421 CAGCCCTGTAAAGCCCGGAGTATGGAACTGTCTCAACAGGCGAGCCAGTGGCCCTGTGT 480
 QY 3853 GCATCTGACGGTGCCTGTGTGGCGGATTCAGACCTCAAGCTGAAGAGCACCCCGCATG 3912
 Db 481 GCATCTGACGGTGCCTGTGTGGCGGATTCAGACCTCAAGCTGAAGAGCACCCCGCATG 540
 QY 3913 CAAGGGAGCGGGGCCAGCTGAATTTTCGGCTTCCCGGTAGCGCCAAATGAGTCAGCTGCG 3972
 Db 541 CAAGGGAGCGGGGCCAGCTGAATTTTCGGCTTCCCGGTAGCGCCAAATGAGTCAGCTGCG 600
 QY 3973 AGCATGTTGAATGGCATGCAGAACACAGGACCCAGTGGGACAGGGGTACCTGGCTACACAG 4032
 Db 601 AGCATGTTGAATGGCATGCAGAACACAGGACCCAGTGGGACAGGGGTACCTGGCTACACAG 660
 QY 4033 CTCTCGGCGACAGCATGCAGACACCCGGGGAGCGCGGCC 4074
 Db 661 CTCTCGGCGACAGCATGCAGACACCCGGGGAGCGCGGCC 702

RESULT 6
 AW953518

LOCUS AW953518 720 bp mRNA linear EST 01-JUN-2000
 DEFINITION ESN365588 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW953518
 VERSION AW953518.1 GI:8143201
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (Bases 1 to 720)
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt,
 I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 51
 Seq primer: Reverse.
 FEATURES
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 /clone_lib="MAGE resequences, MAGB"
 /note="Vector: pBluescriptSKm"
 BASE COUNT 154 a 240 c 211 g 114 t 1 others
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 Best Local Similarity 98.1%; Pred. No. 7.7e-147;
 Matches 705; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
 QY 3271 GTCACCCCTGGAGTCCCTGACCATGACGCTGATGCCAACCTGAACGATGAGATTCTCTG 3330
 Db 1 GTCACCCCTGGAGTCCCTGACCATGACGCTGATGCCAACCTGAACGATGAGATTCTCTG 60
 QY 3331 CGGAGCAGCGTGGTGCAGTATTTAAATTCAGAAACCAAGAGGTTACGACGACGACTTC 3390
 Db 61 CGGAGCAGCGTGGTGCAGTATTTAAATTCAGAAACCAAGAGGTTACGACGACGACTTC 120
 QY 3391 CCCAGCGCCCTCCCGGAGCAGACGAAAGTGGCCCCACGGGCGCGGTGACTTTGACGCGCC 3450
 Db 121 CCCAGCGCCCTCCCGGAGCAGACGAAAGTGGCCCCACGGGCGCGGTGACTTTGACGCGCC 180
 QY 3451 GGGCTGCCAGACAGCCAGCTGGCCAGCAGTTCCATGCGCTCGAGAGCCCTGCCCGAG 3510
 Db 181 GGGCTGCCAGACAGCCAGCTGGCCAGCAGTTCCATGCGCTCGAGAGCCCTGCCCGAG 240
 QY 3511 GGCAGCAAAACCGACTGCCATTCAGTGGAAACGAAGTCAGTCCGGAAGCGCGGACCTG 3570
 Db 241 GGCAGCAAAACCGACTGCCATTCAGTGGAAACGAAGTCAGTCCGGAAGCGCGGACCTG 300
 QY 3571 TCCTCCTCAAGCTCAAAGTGGCGCGCGCGCTGTGCCGAGACTCGGCGCTTTGGG 3630
 Db 301 TCCTCCTCAAGCTCAAAGTGGCGCGCGCGCTGTGCCGAGACTCGGCGCTTTGGG 360
 QY 3631 TTCTCAACGCGCATGGTGTCCACCCGAGAACCCCTTTGAGAGGGGCGCTGCTGGGGG 3690
 Db 361 TTCTCAACGCGCATGGTGTCCACCCGAGAACCCCTTTGAGAGGGGCGCTGCTGGGGG 420
 QY 3691 TATCAGACCTCGGGAGAACCAACCCCTACGCTGGCCGACGAGACTTGTATGCTCCAC 3750
 Db 421 TATCAGACCTCGGGAGAACCAACCCCTACGCTGGCCGACGAGACTTGTATGCTCCAC 480
 QY 3751 AACAGCCCGGAGTGGCAGCAGTGGAAACGCCCTTCCATGAACAGCCCTGTAAAGGCCCG 3810
 Db 481 AACAGCCCGGAGTGGCAGCAGTGGAAACGCCCTTCCATGAACAGCCCTGTAAAGGCCCG 540

QY 3811 CAGTATGGGAAGTGTCTAACAGGAGCAGCGAGTGGCCCTGGTGCACCTCGACGGTGCCTGT 3870
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 Db 541 CAGTATGGGAAGTGTCTAACAGGAGCAGCGAGTGGCCCTGGTGCACCTCGACGGTGCCTGT 600
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 QY 3871 GGTGCGGGGATTCAAGCCTCAAGCTGAGAGACACCCCGCATCGAAGGAGGGGGGCGAC 3930
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 Db 601 GGTGCGGGGATTCAAGCCTCAAGCTGAGAGACACCCCGCATCGAAGGAGGGGGGCGCAA 660
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 QY 3931 CTGAATTCGCGCTCGCGGTAG-CGCCAAATGAGTCAGCTGCGCAGCATGGTGAATGGCA 3988
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RESULT 7
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 LOCUS 788 bp mRNA linear EST 16-OCT-2001
 DEFINITION 603177285F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241692 5',
 mRNA sequence.
 ACCESSION B1915087
 VERSION B1915087.1 GI:16179168
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11609 row: 1 column: 21
 High quality sequence stop: 788.
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 /db_xref="taxon:9606"
 /clone="IMAGE:5241692"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."
 187 a 252 c 182 g 167 t

BASE COUNT
 187 a 252 c 182 g 167 t

ORIGIN
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 Query Match 13.4%; Score 676.8; DB 13; Length 788;
 Best Local Similarity 95.5%; Pred. No. 1.6e-144;
 Matches 718; Conservative 0; Mismatches 32; Indels 2; Gaps 2;
 126 CACTGCAACAGATGTGAGGGAGAAAGCGCTTGCCTCCAGCACCCTTCTAATGAGGATGA 185
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 Db 39 CTCACCAAGAGAGTGTGGCGCAAGTAGCTAGCCAGAGCGCTGGGACCTGTGTAGGATGA 98
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 QY 186 AAGTCTGACAGACTTATCACAGAGAGAGAAACCAATCACTATGACGCCACAGAA 245
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 Db 99 AAGTCTGACAGACTTATCACAGAGAGAGAGAAACCAATCACTATGACGCCACAGAA 158
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 QY 246 TGTCCAGGGGCTCAGCAAGAGTCAGTGAGGAACTTCAACATCGAGTGACGAGAGGGCCTC 305
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159 TGTCCAGGGGCTCAGCAAGTCACTGAGGAACCTTCAACATCGAGTGACGAGAGGGCCTC 218
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 QY 306 ATTGATCAAGAAAGAGATCCATGGTCCCTGCCACACAGTGGCGGAGCCCTCTGTGCCGTA 365
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 Db 219 ATTGATCAAGAAAGAGATCCATGGTCCCTGCCACACAGTGGCGGAGCCCTCTGTGCCGTA 278
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 QY 366 CCGGGGACGGTGTTCCTGACACCCAGCAAGTGGTTACATGAGAGCCACATACACCC 425
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 Db 279 CCGGGGACGGTGTTCCTGACACCCAGCAAGTGGTTACATGAGAGCCACATACACCC 338
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 QY 426 TCCTCATCTTTTCCCTGCCTTCCATCCTCCTGTACCAATTGATGCCAGACATCATGAGGG 485
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 Db 339 TCCTCATCTTTTCCCTGCCTTCCATCCTCCTGTACCAATTGATGCCAGACATCATGAGGG 398
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 QY 486 CCGTTACATTAACATCAATCCGATCCGATTCCTCAATTCATGATGATGATGATGATGATGAT 545
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 QY 546 TAGCCCTACGTATCCGGACCTGCGCTTCATTAGGATCTCCACACAGCAACCCCGCTGC 605
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 Db 459 TAGCCCTACGTATCCGGACCTGCGCTTCATTAGGATCTCCACACAGCAACCCCGCTGC 518
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 QY 606 TGTCTCCGAGTCTCCCTTCAGCCCTCCACATCCCTACATTAATCCCTACATGACTATAT 665
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 Db 519 TGTCTCCGAGTCTCCCTTCAGCCCTCCACATCCCTACATTAATCCCTACATGACTATAT 578
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 QY 666 CCGTCTCTGACAGAGAGCCATCGCTCTCCATGATCTCAGCAACCCCGTGGCTGAGCCC 725
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 Db 579 CCGTCTCTGACAGAGAGCCATCGCTCTCCATGATCTCAGCAACCCCGTGGCTGAGCCC 638
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 QY 726 TACAGATGCGCCCATCGAGAGTCAGCCAGCAGAGATCTATCATCAGATGCGCCCTGCT 785
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 Db 639 TACAGATGCGCCCATCGAGAGTCAGCCAGCAGAGATCTATCATCAGATGCGCCCTGCT 698
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 QY 786 AACTGGCCAGCGCAGCCCTATGACAGACATTAATTCCTCAGCTGCCACCCCGGACGGG 845
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 Db 699 AACTGGCCAGCGCAG-CCCTATGACAGACATTAATTCCTCAGCTGCCACCCCGGACGGG 757
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 QY 846 GGCCATCCATCGAATATCTTCATGCTATGG 877
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 Db 758 GG-CATCCACATGGAATATCTTCATGCTATGG 788
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RESULT 8
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 mRNA sequence.
 ACCESSION B1915087
 VERSION B1915087.1 GI:12759455
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10143 row: p column: 08
 High quality sequence stop: 751.
 Location/Qualifiers
 1. .934

FEATURES
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/clone="IMAGE:3367412"
/clone_lib="NCI CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clones
141920-141791 and 152904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      179 a      142 c      173 g      184 t
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Query Match      12.5%; Score 629.4; DB 12; Length 678;
Best Local Similarity 97.3%; Pred. No. 1.2e-133;
Matches 661; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

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Oy 4431 ATTCTATTTCAGACGGCAGCTGCTGCTATGAGGGGACGAGCGCAAAACCTGAGTT 4490
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Db 618 ATTCTATTTCAGACGGCAGCTGCTGCTATGAGGGGACGAGCGCAAAACCTGAGTT 559
Oy 4491 ACTTCCCGAGTCTATACAGTGCAGACAGCAGTGCAGCCTCGACAGCCATGACCT 4550
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Db 558 ACTTCCCGAGTCTATACAGTGCAGACAGCAGTGCAGCCTCGACAGCCATGACCT 499
Oy 4551 GGAAGGGGTACAGATTCGATCCATATAGAGATGGGAGCAGCAGCTCCAGCTGAT 4610
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Db 498 GGAAGGGGTACAGATTCGATCCATATAGAGATGGGAGCAGCAGCTCCAGCTGAT 439
Oy 4611 GTGGGGGGCCCTGAGCCCAAGTATCAGACCTTCCATAGAGCTCCGCGCTCAC 4670
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Db 438 GTGGGGGGCCCTGAGCCCAAGTATCAGACCTTCCATAGAGCTCCGCGCTCAC 379
Oy 4671 CAGCGCTGGGGCTCCCTCCATCCAGTCCGCTGCTCCATGAGCAGCAGCAACATGGCTA 4730
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Db 378 CAGCGCTGGGGCTCCCTCCATCCAGTCCGCTGCTCCATGAGCAGCAGCAACATGGCTA 320
Oy 4731 TCGGGGACATGATCTTCTGCTGACCTCCCTAGCGGAAAGCAAAATCTCTGCACTTA 4790
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Db 319 TCGGGGACATGATCTTCTGCTGACCTCCCTAGCGGAAAGCAAAATCTCTGCACTTA 260
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Db 259 TGCATATAGCTTTAGGAAAAAAGACACGCAACCAAGCAATTCATAGAGTTGAAGAGA 200
Oy 4851 TTTAACTGACTTTGTTGGCTGTTTGGTCTGATCTGATATATTTTGAACATCTCATCT 4910
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Db 199 TTTAACTGACTTTGTTGGCTGTTTGGTCTGATCTGATATATTTTGAACATCTCATCT 140
Oy 4911 CACCTACTGAGATGTGTTCAATTAATTCCTTTATGAAAGAGACTGGAAGAACCC 4970
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Db 139 CACCTACTGAGATGTGTTCAATTAATTCCTTTATGAAAGAGACTGGAAGAACCC 80
Oy 4971 TAAATATTCAGGAGAAAGTGTCTTCATTTGAGTTTGAATGAGATTTGTTACACTC 5030
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Db 79 TAAATATTCAGGAGAAAGTGTCTTCATTTGAGTTTGAATGAGATTTGTTACACTC 20
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RESULT 12
BQ447085/c

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LOCUS      BQ447085      694 bp      mRNA      linear      EST 29-MAY-2002
DEFINITION UI-H-EU1-bad-g-19-0-UI-s1 NCI-CGAP_Ctl Homo sapiens CDNA clone
ACCESSION  BQ447085
VERSION    BQ447085.1  GI:21250197
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 694)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            CDNA library preparation: Dr. M. Bento Soares, University of Iowa
            CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            The following repetitive elements were found in this CDNA
            sequence: 61-83, >AT-rich#Low-complexity (matched complement)
            Seq primer: M13 FORWARD
            POLYA=yes.

FEATURES             Location/Qualifiers
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                     /clone_lib="NCI CGAP_Ctl"
                     /tissue_type="Osteoarthritic Cartilage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Knee; Vector: pT73-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     NCI CGAP_Ctl is a normalized CDNA library containing the
                     following tissue(s): Osteoarthritic Cartilage The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT73-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGCATCAGCT.
                     TAG_LIB-UI-H-EU1
                     TAG_TISSUE=osteoarthritis cartilage
                     TAG_SEQ=TCATCAGCT"

BASE COUNT      174 a      138 c      171 g      210 t      1 others
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Query Match      11.8%; Score 598.4; DB 14; Length 694;
Best Local Similarity 99.5%; Pred. No. 1.6e-126;
Matches 610; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 501 GAGCCCAAGATCATTCAGACCTTCCCATAGCTCTCCGCTCAGCAGCGCTGGGC 442

Qy 4683 GTCCCTCCCATTCGCCAGTGTCTCATGAGACACCAACATGGCTATGGGACATGA 4742

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Qy 4743 GTTCCTTGCAGACCTCCCTAGGGAAGAAAGCAATTCCTTCAGTATGCAATGAGCTT 4802

Db 382 GTTCCTTGCAGACCTCCCTAGGGAAGAAAGCAATTCCTTCAGTATGCAATGAGCTT 323

Qy 4803 TAGGAAAAAAGAGCTCAACCAACGGAATTCATAGAGTTGAAGAGATTAAGTACTT 4862

Db 322 TAGGAAAAAAGAGCTCAACCAACGGAATTCATAGAGTTGAAGAGATTAAGTACTT 263

Qy 4863 TGTTCCTGCTGTTTTTTAGTCTGTATGATTTTATGCAATCTCATCTACTACTGAG 4922

Db 262 TGTTCCTGCTGTTTTTTAGTCTGTATGATTTTATGCAATCTCATCTACTACTGAG 203

Qy 4923 ATGTGTTCAATATATATTCCTTTATGAAAAAGACTCTGAAAAACCTTAAGTATCTTA 4982

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RESULT 13
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VERSION BE21252.1 GI:8908570
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SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 576)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov

JOURNAL COMMENT
REFERENCE
AUTHORS
TITLE
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL, send email to: info@image.llnl.gov
Seq primer: -400P from G1bco
High quality sequence stop: 404.
Location/Qualifiers
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/lab_host="DH10B"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: SalI, Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

BASE COUNT 156 a 118 c 144 g 156 t 2 others
ORIGIN

Query Match 11.1%; Score 563; DB 10; Length 576;
Best Local Similarity 99.5%; Pred. No. 2e-118;
Matches 574; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 576 AGCGCAAAACCTGACTTCTTCCCGAGTCTATATCATGATGACAGACAGTGGAC 517

Qy 4531 AGCGCAAAACCTGACTTCTTCCCGAGTCTATATCATGATGACAGACAGTGGAC 4590

Db 516 AGCGCAAAACCTGACTTCTTCCCGAGTCTATATCATGATGACAGACAGTGGAC 457

Qy 4591 GGGGACCACTCCAGCTGATGTCGGGGCCCTGAGCCCAAGTATCATTCAGAACCTTTC 4650

Db 456 GGGGACCACTCCAGCTGATGTCGGGGCCCTGAGCCCAAGTATCATTCAGAACCTTTC 397

Qy 4651 CATAGCTCTCCCGCTCAGCAGCGCTCGGGCGTCCCTCCATTCAGTCCGCTGCTCAT 4710

Db 396 CATAGCTCTCCCGCTCAGCAGCGCTCGGGCGTCCCTCCATTCAGTCCGCTGCTCAT 338

Qy 4711 GAGCACCAACATGCTATCGGGGACATGATGTTCTTGTGACTCCCTAGCGGAGA 4770

Db 337 GAGCACCAACATGCTATCGGGGACATGATGTTCTTGTGACTCCCTAGCGGAGA 278

Qy 4771 AAGCAATTCCTTCGAGTTATGCAATAGCTTTAGAAAAAAGAGCTGCAACCAAGGAA 4830

Db 277 AAGCAATTCCTTCGAGTTATGCAATAGCTTTAGAAAAAAGAGCTGCAACCAAGGAA 218

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RESULT 14
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ACCESSION A1796831
VERSION A1796831.1 GI:5362294
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SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 650)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov

JOURNAL COMMENT
REFERENCE
AUTHORS
TITLE
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

Copied from PCIUS2003092 on 04-03-2004

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Db 214 CATAGGAGTTGAAGAGATTAACTGACTTTGTTGGCTGTTTATAGTTCGTATG 155
QY 4892 TATTTAGCAATCTCATCTCACCCTAAGATGCTTCAATTATATCTTTATGSA 4951
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QY 5012 AATCAGTATTTGTACATCAACCAACCCCTCTTT 5045
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Search completed: December 11, 2002, 00:29:40
Job time : 4311 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 02:29:06 ; Search time 110 Seconds
(without alignments)
14093.191 Million cell updates/sec

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Perfect score: 5055
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	27.4	0.5	99	4	US-08-542-634-12
6	27.4	0.5	99	4	US-08-477-292-12
7	27.4	0.5	99	5	PCT-US95-13703-12
8	27	0.5	96	4	US-09-242-095-26
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141	23.2	0.5	90	4	US-09-461-697-434	Sequence 434, App	c 214	22.6	0.4	75	1	US-08-750-419A-4	Sequence 4, App1
142	23.2	0.5	91	2	US-09-205-995-69	Sequence 69, App1	c 215	22.6	0.4	78	6	US-08-318-193-72	Sequence 72, App1
143	23.2	0.5	97	2	US-08-479-729-7	Sequence 7, App1	c 216	22.6	0.4	93	2	5457037-7	Sequence 7, App1
144	23.2	0.5	97	5	PCT-US96-08089-7	Sequence 7, App1	c 217	22.6	0.4	93	3	US-08-707-237A-100	Sequence 100, App
145	23.2	0.5	98	1	US-07-889-651-16	Sequence 16, App1	c 218	22.6	0.4	93	3	US-08-642-246-22	Sequence 22, App1
146	23.2	0.5	100	1	US-07-797-556-7	Sequence 7, App1	c 219	22.6	0.4	93	4	US-08-806-029-20	Sequence 20, App1
147	23	0.5	66	4	US-08-556-978B-42	Sequence 42, App1	c 220	22.6	0.4	93	4	US-09-451-206-22	Sequence 22, App1
148	23	0.5	68	1	US-08-180-195-26	Sequence 26, App1	c 221	22.6	0.4	93	5	PCT-US96-06229-22	Sequence 22, App1
149	23	0.5	68	1	US-08-477-329-26	Sequence 26, App1	c 222	22.6	0.4	96	1	US-08-208-886C-60	Sequence 60, App1
150	23	0.5	68	2	US-08-475-458-26	Sequence 26, App1	c 223	22.6	0.4	96	1	US-08-208-886C-72	Sequence 72, App1
151	23	0.5	68	3	US-08-980-400-26	Sequence 26, App1	c 224	22.6	0.4	96	1	US-08-704-744-60	Sequence 60, App1
152	23	0.5	68	4	US-09-583-459A-26	Sequence 26, App1	c 225	22.6	0.4	96	1	US-08-704-744-60	Sequence 72, App1
153	23	0.5	68	4	US-09-583-459A-26	Sequence 26, App1	c 226	22.6	0.4	96	1	US-08-469-557-60	Sequence 60, App1
154	23	0.5	68	4	US-09-583-459A-26	Sequence 26, App1	c 227	22.6	0.4	96	2	US-08-290-799B-60	Sequence 60, App1
155	23	0.5	68	4	US-09-583-459A-26	Sequence 26, App1	c 228	22.6	0.4	97	3	US-08-825-852-38	Sequence 38, App1
156	23	0.5	82	2	US-08-476-176B-24	Sequence 24, App1	c 229	22.6	0.4	97	3	US-08-825-852-38	Sequence 38, App1
157	23	0.5	82	3	US-08-127-721A-24	Sequence 24, App1	c 230	22.6	0.4	97	4	US-09-052-888-44	Sequence 44, App1
158	23	0.5	82	3	US-08-485-246A-24	Sequence 24, App1	c 231	22.6	0.4	97	4	US-09-052-888-44	Sequence 44, App1
159	23	0.5	89	2	US-08-481-658B-42	Sequence 42, App1	c 232	22.6	0.4	100	1	US-08-208-886C-59	Sequence 59, App1
160	23	0.5	89	2	US-08-477-504A-42	Sequence 42, App1	c 233	22.6	0.4	100	1	US-08-208-886C-71	Sequence 71, App1
161	23	0.5	89	2	US-08-486-756A-42	Sequence 42, App1	c 234	22.6	0.4	100	1	US-08-704-744-59	Sequence 59, App1
162	23	0.5	89	2	US-08-485-862B-42	Sequence 42, App1	c 235	22.6	0.4	100	1	US-08-704-744-59	Sequence 59, App1
163	23	0.5	89	3	US-08-87-739-42	Sequence 42, App1	c 236	22.6	0.4	100	2	US-08-469-557-59	Sequence 59, App1
164	23	0.5	89	3	US-08-487-077A-42	Sequence 42, App1	c 237	22.4	0.4	60	5	PCT-US93-01901-27	Sequence 27, App1
165	23	0.5	89	3	US-08-485-863A-42	Sequence 42, App1	c 238	22.4	0.4	69	4	US-09-042-353-246	Sequence 246, App
166	23	0.5	89	4	US-08-485-049D-42	Sequence 42, App1	c 239	22.4	0.4	69	4	US-08-758-417A-94	Sequence 94, App1
167	23	0.5	89	4	US-09-177-776-42	Sequence 42, App1	c 240	22.4	0.4	72	1	US-07-826-928A-19	Sequence 19, App1
168	23	0.5	89	4	US-09-177-776-42	Sequence 42, App1	c 241	22.4	0.4	81	3	US-08-776-251-2	Sequence 2, App1
169	23	0.5	96	1	US-08-447-422-11	Sequence 11, App1	c 242	22.4	0.4	81	4	US-08-556-978B-90	Sequence 90, App1
170	23	0.5	96	1	US-08-755-587-4	Sequence 4, App1	c 243	22.4	0.4	81	4	US-09-497-933A-20	Sequence 20, App1
171	23	0.5	97	3	US-08-825-852-39	Sequence 39, App1	c 244	22.4	0.4	95	2	US-08-476-176B-20	Sequence 20, App1
172	23	0.5	97	3	US-08-825-852-40	Sequence 40, App1	c 245	22.4	0.4	95	2	US-08-127-721A-20	Sequence 20, App1
173	23	0.5	97	3	US-08-825-852-43	Sequence 43, App1	c 246	22.4	0.4	95	3	US-08-485-246A-20	Sequence 20, App1

247	22.4	0.4	96	1	US-08-447-422-12	Sequence 12, Appl	320	21.6	0.4	88	6	5194596-6	Patent No. 5194596
248	22.4	0.4	100	2	US-08-690-495-30	Sequence 30, Appl	321	21.6	0.4	94	4	US-09-025-769B-175	Sequence 175, Appl
249	22.4	0.4	100	2	US-08-690-494-30	Sequence 30, Appl	322	21.4	0.4	62	1	US-08-182-175A-98	Sequence 98, Appl
250	22.4	0.4	100	5	PCT-US95-07671-30	Sequence 30, Appl	323	21.4	0.4	62	1	US-08-446-908-15	Sequence 15, Appl
C 251	22.2	0.4	57	1	US-07-609-716-51	Sequence 51, Appl	324	21.4	0.4	62	1	US-08-231-205A-87	Sequence 87, Appl
C 252	22.2	0.4	57	1	US-07-609-716-52	Sequence 52, Appl	325	21.4	0.4	62	1	US-08-474-633A-17	Sequence 17, Appl
C 253	22.2	0.4	57	3	US-08-642-255-20	Sequence 20, Appl	326	21.4	0.4	62	2	US-08-871-161-15	Sequence 15, Appl
C 254	22.2	0.4	57	3	US-08-475-411A-51	Sequence 51, Appl	327	21.4	0.4	62	4	US-08-823-771-87	Sequence 87, Appl
C 255	22.2	0.4	57	3	US-08-475-411A-52	Sequence 52, Appl	328	21.4	0.4	62	5	PCT-US92-06412-98	Sequence 98, Appl
C 256	22.2	0.4	57	4	US-08-478-029A-51	Sequence 51, Appl	329	21.4	0.4	62	5	US-08-468-161-102	Sequence 102, Appl
C 257	22.2	0.4	57	4	US-08-478-029A-52	Sequence 52, Appl	330	21.4	0.4	69	3	US-09-273-685-102	Sequence 102, Appl
C 258	22.2	0.4	64	4	US-09-025-769B-110	Sequence 110, Appl	331	21.4	0.4	69	5	PCT-US95-11934-102	Sequence 102, Appl
C 259	22.2	0.4	67	2	US-07-977-284A-218	Sequence 218, Appl	332	21.4	0.4	75	1	US-08-237-716-5	Sequence 5, Appl
C 260	22.2	0.4	72	1	US-08-256-426B-218	Sequence 218, Appl	333	21.4	0.4	75	1	US-08-237-716-6	Sequence 6, Appl
C 261	22.2	0.4	72	1	US-08-318-193-78	Sequence 78, Appl	C 334	21.4	0.4	75	3	US-09-131-567-2	Sequence 2, Appl
C 262	22.2	0.4	81	4	US-08-556-978B-91	Sequence 91, Appl	C 335	21.4	0.4	79	1	US-08-384-708A-226	Sequence 226, Appl
C 263	22.2	0.4	90	3	US-08-952-664-17	Sequence 17, Appl	C 336	21.4	0.4	79	2	US-08-470-939-22	Sequence 22, Appl
C 264	22.2	0.4	90	4	US-09-065-058-16	Sequence 16, Appl	C 337	21.4	0.4	79	4	US-08-687-421-118	Sequence 118, Appl
C 265	22.2	0.4	90	4	US-09-487-874-17	Sequence 17, Appl	C 338	21.4	0.4	79	5	PCT-US96-09452-22	Sequence 22, Appl
C 266	22.2	0.4	91	4	US-09-404-879A-201	Sequence 201, Appl	C 339	21.4	0.4	85	2	US-08-852-807-8	Sequence 8, Appl
C 267	22.2	0.4	92	1	US-08-487-141B-109	Sequence 109, Appl	C 340	21.4	0.4	87	2	US-08-476-176B-22	Sequence 22, Appl
C 268	22.2	0.4	52	3	US-08-718-904-104	Sequence 104, Appl	C 341	21.4	0.4	87	3	US-08-127-721A-22	Sequence 22, Appl
C 269	22.2	0.4	55	1	US-07-826-928A-16	Sequence 16, Appl	C 342	21.4	0.4	87	3	US-08-485-246A-22	Sequence 22, Appl
C 270	22.2	0.4	66	1	US-08-180-195-23	Sequence 23, Appl	C 343	21.4	0.4	92	1	US-08-130-827-94	Sequence 94, Appl
C 271	22.2	0.4	66	1	US-08-477-329-23	Sequence 23, Appl	C 344	21.4	0.4	92	1	US-08-478-675-94	Sequence 94, Appl
C 272	22.2	0.4	66	2	US-08-475-458-23	Sequence 23, Appl	C 345	21.4	0.4	94	1	US-08-479-783A-59	Sequence 59, Appl
C 273	22.2	0.4	66	2	US-08-980-400-23	Sequence 23, Appl	C 346	21.4	0.4	94	1	US-08-479-725-59	Sequence 59, Appl
C 274	22.2	0.4	66	4	US-09-583-459A-23	Sequence 23, Appl	C 347	21.4	0.4	94	1	US-08-618-693-59	Sequence 59, Appl
C 275	22.2	0.4	66	4	US-09-583-210-23	Sequence 23, Appl	C 348	21.4	0.4	94	4	US-08-973-124-148	Sequence 148, Appl
C 276	22.2	0.4	66	4	US-09-583-449A-23	Sequence 23, Appl	C 349	21.4	0.4	94	4	US-08-991-743C-59	Sequence 59, Appl
C 277	22.2	0.4	67	4	US-09-435-059-23	Sequence 23, Appl	C 350	21.4	0.4	94	5	PCT-US96-08014-148	Sequence 148, Appl
C 278	22.2	0.4	67	4	US-07-977-284A-245	Sequence 245, Appl	C 351	21.4	0.4	97	2	US-08-476-176B-25	Sequence 25, Appl
C 279	22.2	0.4	67	2	US-08-256-426B-245	Sequence 245, Appl	C 352	21.4	0.4	97	2	US-08-127-721A-25	Sequence 25, Appl
C 280	22.2	0.4	68	1	US-08-440-787A-52	Sequence 52, Appl	C 353	21.4	0.4	97	3	US-08-485-246A-25	Sequence 25, Appl
C 281	22.2	0.4	68	4	US-08-367-685-52	Sequence 52, Appl	C 354	21.4	0.4	97	3	US-08-825-852-11	Sequence 11, Appl
C 282	22.2	0.4	68	5	PCT-US91-07141-52	Sequence 52, Appl	C 355	21.4	0.4	97	3	US-08-825-852-12	Sequence 12, Appl
C 283	22.2	0.4	76	4	US-07-757-022B-3	Sequence 3, Appl	C 356	21.4	0.4	97	3	US-08-825-852-14	Sequence 14, Appl
C 284	22.2	0.4	81	4	US-08-170-290A-17	Sequence 17, Appl	C 357	21.4	0.4	97	4	US-09-052-888-11	Sequence 11, Appl
C 285	22.2	0.4	84	2	US-08-426-599B-10	Sequence 10, Appl	C 358	21.4	0.4	97	4	US-09-052-888-42	Sequence 42, Appl
C 286	22.2	0.4	89	2	US-08-716-308-4	Sequence 4, Appl	C 359	21.4	0.4	97	4	US-09-052-888-44	Sequence 44, Appl
C 287	22.2	0.4	92	4	US-09-506-729-48	Sequence 48, Appl	C 360	21.4	0.4	100	3	US-09-017-631-34	Sequence 34, Appl
C 288	22.2	0.4	95	4	US-09-511-625B-44	Sequence 44, Appl	C 361	21.4	0.4	100	4	US-09-018-138-12	Sequence 12, Appl
C 289	22.2	0.4	95	4	US-08-464-700-43	Sequence 43, Appl	C 362	21.2	0.4	60	4	US-09-284-627-14	Sequence 14, Appl
C 290	21.8	0.4	45	5	US-08-522-623-4	Sequence 4, Appl	C 363	21.2	0.4	64	2	US-08-874-678-13	Sequence 13, Appl
C 291	21.8	0.4	45	5	PCT-US93-03256-4	Sequence 4, Appl	C 364	21.2	0.4	64	3	US-08-643-839-43	Sequence 43, Appl
C 292	21.8	0.4	67	1	US-07-977-284A-258	Sequence 258, Appl	C 365	21.2	0.4	64	4	US-09-348-866-43	Sequence 43, Appl
C 293	21.8	0.4	67	2	US-08-256-426B-258	Sequence 258, Appl	C 366	21.2	0.4	69	1	US-08-215-138-3	Sequence 3, Appl
C 294	21.8	0.4	75	1	US-07-982-712-6	Sequence 6, Appl	C 367	21.2	0.4	73	4	US-08-407-344-3	Sequence 4, Appl
C 295	21.8	0.4	75	1	US-07-941-651-5	Sequence 5, Appl	C 368	21.2	0.4	73	4	US-09-303-069-20	Sequence 20, Appl
C 296	21.8	0.4	75	1	US-08-279-966-5	Sequence 5, Appl	C 369	21.2	0.4	73	4	US-09-134-250-20	Sequence 20, Appl
C 297	21.8	0.4	75	1	US-08-482-111-61	Sequence 61, Appl	C 370	21.2	0.4	82	2	US-08-481-658B-37	Sequence 37, Appl
C 298	21.8	0.4	83	1	US-08-175-135-35	Sequence 35, Appl	C 371	21.2	0.4	82	2	US-08-477-504A-37	Sequence 37, Appl
C 299	21.8	0.4	83	1	US-08-477-509B-70	Sequence 70, Appl	C 372	21.2	0.4	82	2	US-08-486-756A-37	Sequence 37, Appl
C 300	21.8	0.4	83	2	US-08-707-237A-41	Sequence 41, Appl	C 373	21.2	0.4	82	2	US-08-485-862B-37	Sequence 37, Appl
C 301	21.8	0.4	83	3	US-08-482-085B-70	Sequence 70, Appl	C 374	21.2	0.4	82	3	US-08-787-729-37	Sequence 37, Appl
C 302	21.8	0.4	83	4	US-09-444-791A-70	Sequence 70, Appl	C 375	21.2	0.4	82	3	US-08-487-077A-37	Sequence 37, Appl
C 303	21.8	0.4	86	2	US-08-870-518-12	Sequence 12, Appl	C 376	21.2	0.4	82	3	US-08-485-863A-37	Sequence 37, Appl
C 304	21.8	0.4	89	4	US-09-296-328A-2	Sequence 2, Appl	C 377	21.2	0.4	82	4	US-08-485-049D-37	Sequence 37, Appl
C 305	21.8	0.4	89	4	US-08-464-700-18	Sequence 18, Appl	C 378	21.2	0.4	82	4	US-09-177-776-37	Sequence 37, Appl
C 306	21.6	0.4	54	1	US-07-982-712-18	Sequence 18, Appl	C 379	21.2	0.4	82	4	US-09-177-776-37	Sequence 37, Appl
C 307	21.6	0.4	54	1	US-09-339-913B-52	Sequence 52, Appl	C 380	21.2	0.4	86	1	US-08-447-169A-218	Sequence 218, Appl
C 308	21.6	0.4	59	4	US-09-339-904A-52	Sequence 52, Appl	C 381	21.2	0.4	87	1	US-08-433-126A-180	Sequence 180, Appl
C 309	21.6	0.4	59	4	US-08-769-062B-52	Sequence 52, Appl	C 382	21.2	0.4	87	1	US-08-433-126A-180	Sequence 180, Appl
C 310	21.6	0.4	59	4	US-09-344-002B-52	Sequence 52, Appl	C 383	21.2	0.4	87	3	US-08-976-413A-180	Sequence 180, Appl
C 311	21.6	0.4	60	3	US-09-559-565C-52	Sequence 52, Appl	C 384	21.2	0.4	87	4	US-08-936-477-4	Sequence 4, Appl
C 312	21.6	0.4	60	3	US-08-654-623-14	Sequence 14, Appl	C 385	21.2	0.4	87	4	US-09-113-785-13	Sequence 13, Appl
C 313	21.6	0.4	64	4	US-09-025-769B-102	Sequence 102, Appl	C 386	21.2	0.4	87	5	PCT-US96-06059-180	Sequence 180, Appl
C 314	21.6	0.4	64	4	US-08-931-858B-209	Sequence 209, Appl	C 387	21.2	0.4	90	4	US-08-974-549A-667	Sequence 667, Appl
C 315	21.6	0.4	69	4	US-08-931-858B-210	Sequence 210, Appl	C 388	21.2	0.4	90	4	US-08-974-549A-668	Sequence 668, Appl
C 316	21.6	0.4	70	4	US-09-625-188-41	Sequence 41, Appl	C 389	21.2	0.4	93	2	US-08-553-501A-47	Sequence 47, Appl
C 317	21.6	0.4	72	4	US-09-404-879A-304	Sequence 304, Appl	C 390	21.2	0.4	93	3	US-09-205-231-47	Sequence 47, Appl
C 318	21.6	0.4	81	3	US-09-014-416-57	Sequence 57, Appl	C 391	21	0.4	29	4	US-09-657-042A-6	Sequence 6, Appl
C 319	21.6	0.4	84	4	US-08-943-731-204	Sequence 204, Appl	C 392	21	0.4	41	1	US-08-253-155A-82	Sequence 82, Appl

C 393	21	0.4	41	1	US-08-625-209A-11	Sequence 11, App1	466	21	0.4	93	5	PCT-US92-10983-133	Sequence 133, App
C 394	21	0.4	41	3	US-08-853-733B-11	Sequence 11, App1	C 467	21	0.4	94	1	US-07-626-618A-14	Sequence 14, App1
C 395	21	0.4	45	4	US-09-561-490E-35	Sequence 35, App1	C 468	21	0.4	94	1	US-07-928-611A-14	Sequence 14, App1
C 396	21	0.4	47	4	US-09-641-638-877	Sequence 877, App	C 469	21	0.4	94	1	US-08-333-977-14	Sequence 14, App1
C 397	21	0.4	64	1	US-08-053-131-135	Sequence 135, App	C 470	21	0.4	94	1	US-08-053-131-144	Sequence 144, App
C 398	21	0.4	64	1	US-08-645-641-135	Sequence 135, App	C 471	21	0.4	94	1	US-08-645-641-144	Sequence 144, App
C 399	21	0.4	64	1	US-07-853-408B-135	Sequence 135, App	C 472	21	0.4	94	1	US-07-853-408B-144	Sequence 144, App
C 400	21	0.4	64	1	US-08-096-762-135	Sequence 135, App	C 473	21	0.4	94	1	US-08-096-762-144	Sequence 144, App
C 401	21	0.4	64	2	US-08-308-865-135	Sequence 135, App	C 474	21	0.4	94	2	US-08-308-865-144	Sequence 144, App
C 402	21	0.4	64	2	US-09-042-353-252	Sequence 252, App	C 475	21	0.4	94	2	US-08-487-811A-14	Sequence 144, App
C 403	21	0.4	64	4	US-08-758-417A-100	Sequence 100, App	C 476	21	0.4	94	4	US-09-060-694-14	Sequence 14, App1
C 404	21	0.4	64	5	PCT-US92-10983-135	Sequence 135, App	C 477	21	0.4	94	4	US-09-042-353-261	Sequence 14, App1
C 405	21	0.4	65	4	US-09-142-355B-8	Sequence 8, App11	C 478	21	0.4	94	4	US-08-758-417A-109	Sequence 109, App
C 406	21	0.4	72	1	US-08-208-886C-56	Sequence 56, App1	C 479	21	0.4	94	4	US-09-378-074-14	Sequence 14, App1
C 407	21	0.4	72	1	US-08-704-744-56	Sequence 56, App1	C 480	21	0.4	94	5	PCT-US92-10983-144	Sequence 144, App
C 408	21	0.4	72	1	US-08-469-557-56	Sequence 56, App1	C 481	21	0.4	94	5	PCT-US93-07370-14	Sequence 14, App
C 409	21	0.4	72	2	US-08-290-793B-56	Sequence 56, App1	C 482	21	0.4	94	5	US-09-042-353-245	Sequence 245, App
C 410	21	0.4	73	2	US-09-010-928B-8	Sequence 8, App11	C 483	21	0.4	99	4	US-08-758-417A-93	Sequence 93, App1
C 411	21	0.4	74	3	US-08-789-333F-61	Sequence 61, App1	C 484	21	0.4	36	1	US-08-309-512-60	Sequence 60, App1
C 412	21	0.4	74	4	US-08-787-738B-61	Sequence 61, App1	C 485	20.8	0.4	42	4	US-09-250-609-34	Sequence 34, App1
C 413	21	0.4	76	1	US-08-208-886C-55	Sequence 55, App1	C 486	20.8	0.4	45	5	US-09-250-609-34	Sequence 34, App1
C 414	21	0.4	76	1	US-08-704-744-55	Sequence 55, App1	C 487	20.8	0.4	47	4	PCT-US95-14639-8	Sequence 8, App1
C 415	21	0.4	76	1	US-08-469-557-55	Sequence 55, App1	C 488	20.8	0.4	54	1	US-08-015-180-8	Sequence 8, App1
C 416	21	0.4	76	2	US-08-290-793B-55	Sequence 55, App1	C 489	20.8	0.4	54	1	US-08-649-196-8	Sequence 8, App1
C 417	21	0.4	78	4	US-08-976-183A-1	Sequence 1, App11	C 490	20.8	0.4	60	3	US-08-983-607-14	Sequence 14, App1
C 418	21	0.4	78	4	US-09-543-004-36	Sequence 36, App1	C 491	20.8	0.4	61	1	US-08-616-133-22	Sequence 22, App1
C 419	21	0.4	78	4	US-09-425-638A-36	Sequence 36, App1	C 492	20.8	0.4	61	1	US-08-802-985-22	Sequence 22, App1
C 420	21	0.4	80	1	US-08-543-004-36	Sequence 36, App1	C 493	20.8	0.4	65	1	US-08-616-133-21	Sequence 21, App1
C 421	21	0.4	80	1	US-08-208-886C-36	Sequence 36, App1	C 494	20.8	0.4	65	1	US-08-802-985-21	Sequence 21, App1
C 422	21	0.4	80	1	US-08-704-744-36	Sequence 36, App1	C 495	20.8	0.4	66	4	US-08-556-978B-41	Sequence 41, App1
C 423	21	0.4	80	1	US-08-469-557-36	Sequence 36, App1	C 496	20.8	0.4	67	2	US-07-977-284A-23	Sequence 23, App
C 424	21	0.4	80	2	US-08-290-793B-36	Sequence 36, App1	C 497	20.8	0.4	67	2	US-08-256-426B-36	Sequence 223, App
C 425	21	0.4	80	4	US-08-978-806-6	Sequence 6, App11	C 498	20.8	0.4	68	1	US-08-428-733A-50	Sequence 50, App1
C 426	21	0.4	81	1	US-08-238-863-22	Sequence 22, App1	C 499	20.8	0.4	72	1	US-07-977-284A-29	Sequence 229, App
C 427	21	0.4	81	1	US-08-238-863-45	Sequence 45, App1	C 500	20.8	0.4	72	2	US-08-256-426B-29	Sequence 229, App
C 428	21	0.4	81	1	US-08-443-407-22	Sequence 22, App1	C 501	20.8	0.4	73	1	US-07-854-845B-2	Sequence 2, App11
C 429	21	0.4	81	1	US-08-443-407-45	Sequence 45, App1	C 502	20.8	0.4	77	3	US-08-666-354A-10	Sequence 10, App1
C 430	21	0.4	81	5	PCT-US95-05600-166	Sequence 166, App	C 503	20.8	0.4	80	1	US-08-290-373B-13	Sequence 13, App1
C 431	21	0.4	81	5	PCT-US95-05600-189	Sequence 189, App	C 504	20.8	0.4	81	4	US-08-556-978B-27	Sequence 27, App1
C 432	21	0.4	84	2	US-08-788-943A-14	Sequence 14, App1	C 505	20.8	0.4	81	4	US-08-556-978B-28	Sequence 28, App1
C 433	21	0.4	84	5	PCT-US96-00952-15	Sequence 15, App1	C 506	20.8	0.4	81	4	US-09-497-933A-20	Sequence 20, App1
C 434	21	0.4	86	1	US-08-433-126A-69	Sequence 69, App1	C 507	20.8	0.4	82	1	US-08-290-373B-14	Sequence 14, App1
C 435	21	0.4	86	1	US-08-433-126A-69	Sequence 69, App1	C 508	20.8	0.4	83	4	US-09-133-321-10	Sequence 10, App1
C 436	21	0.4	86	3	US-08-976-413A-69	Sequence 69, App1	C 509	20.8	0.4	86	4	US-08-974-751A-27	Sequence 27, App1
C 437	21	0.4	86	5	PCT-US96-06059-69	Sequence 69, App1	C 510	20.8	0.4	90	4	US-08-556-978B-73	Sequence 73, App1
C 438	21	0.4	87	2	US-08-788-943A-15	Sequence 15, App1	C 511	20.8	0.4	90	4	US-08-481-658B-32	Sequence 32, App1
C 439	21	0.4	87	2	US-08-449-287-19	Sequence 19, App1	C 512	20.8	0.4	90	4	US-08-556-978B-74	Sequence 74, App1
C 440	21	0.4	87	5	PCT-US96-00952-16	Sequence 16, App1	C 513	20.8	0.4	92	1	US-08-353-400-19	Sequence 19, App1
C 441	21	0.4	88	4	US-09-335-012-25	Sequence 25, App1	C 514	20.8	0.4	93	2	US-08-481-658B-32	Sequence 32, App1
C 442	21	0.4	88	4	US-09-941-964-25	Sequence 25, App1	C 515	20.8	0.4	93	2	US-08-477-504A-32	Sequence 32, App1
C 443	21	0.4	88	6	5219739-6	Sequence 25, App1	C 516	20.8	0.4	93	2	US-08-486-756A-32	Sequence 32, App1
C 444	21	0.4	90	4	US-08-464-700-41	Sequence 41, App1	C 517	20.8	0.4	93	2	US-08-485-865B-32	Sequence 32, App1
C 445	21	0.4	90	4	US-08-556-978B-74	Sequence 74, App1	C 518	20.8	0.4	93	2	US-08-787-733B-32	Sequence 32, App1
C 446	21	0.4	90	4	US-09-480-251-10	Sequence 10, App1	C 519	20.8	0.4	93	3	US-08-487-077A-32	Sequence 32, App1
C 447	21	0.4	92	1	US-08-319-467-5	Sequence 5, App11	C 520	20.8	0.4	93	3	US-08-485-865A-32	Sequence 32, App1
C 448	21	0.4	92	2	US-08-781-084-5	Sequence 5, App11	C 521	20.8	0.4	93	3	US-08-485-865A-32	Sequence 32, App1
C 449	21	0.4	92	5	PCT-US95-12914-5	Sequence 5, App11	C 522	20.8	0.4	93	4	US-09-178-115-32	Sequence 32, App1
C 450	21	0.4	93	1	US-08-458-120-3	Sequence 3, App11	C 523	20.8	0.4	93	4	US-09-177-776-32	Sequence 32, App1
C 451	21	0.4	93	1	US-08-053-131-133	Sequence 133, App	C 524	20.8	0.4	95	2	US-08-596-387B-103	Sequence 103, App
C 452	21	0.4	93	1	US-08-353-400-20	Sequence 20, App1	C 525	20.8	0.4	95	4	US-09-067-615-103	Sequence 103, App
C 453	21	0.4	93	1	US-08-645-641-133	Sequence 133, App	C 526	20.8	0.4	95	5	PCT-US95-09816A-103	Sequence 103, App
C 454	21	0.4	93	1	US-07-853-408B-133	Sequence 133, App	C 527	20.8	0.4	98	1	US-08-088-656-42	Sequence 42, App1
C 455	21	0.4	93	1	US-08-096-762-133	Sequence 133, App	C 528	20.8	0.4	98	2	US-08-471-907A-42	Sequence 42, App1
C 456	21	0.4	93	2	US-08-308-865-133	Sequence 133, App	C 529	20.8	0.4	99	2	US-08-381-657-30	Sequence 30, App1
C 457	21	0.4	93	2	US-08-187-186A-3	Sequence 3, App11	C 530	20.8	0.4	100	1	US-08-129-930B-90	Sequence 90, App1
C 458	21	0.4	93	2	US-08-442-497C-3	Sequence 3, App11	C 531	20.8	0.4	100	3	US-08-431-081B-13	Sequence 13, App1
C 459	21	0.4	93	4	US-09-042-353-250	Sequence 250, App	C 532	20.8	0.4	100	3	US-08-608-016-13	Sequence 13, App1
C 460	21	0.4	93	4	US-08-556-978B-24	Sequence 24, App1	C 533	20.8	0.4	100	4	US-08-134-346A-45	Sequence 45, App1
C 461	21	0.4	93	4	US-08-556-978B-25	Sequence 25, App1	C 534	20.8	0.4	100	4	US-08-976-288A-90	Sequence 90, App1
C 462	21	0.4	93	4	US-08-556-978B-87	Sequence 87, App1	C 535	20.8	0.4	100	4	US-09-497-933A-13	Sequence 13, App1
C 463	21	0.4	93	4	US-08-556-978B-88	Sequence 88, App1	C 536	20.8	0.4	100	4	US-09-298-886-20	Sequence 20, App1
C 464	21	0.4	93	4	US-08-758-417A-98	Sequence 98, App1	C 537	20.6	0.4	27	3	US-08-594-455-58	Sequence 58, App1
C 465	21	0.4	93	4	US-09-333-033-3	Sequence 3, App11	C 538	20.6	0.4	27	3	US-09-258-408-58	Sequence 58, App1

C 539	20.6	0.4	31	2	US-08-560-916-3	Sequence 3, Appl1	612	20.6	0.4	96	3	US-08-836-561-72	Sequence 72, Appl1
C 540	20.6	0.4	31	2	US-08-676-841-30	Sequence 3, Appl1	613	20.6	0.4	96	3	US-08-484-322-6	Sequence 6, Appl1
C 541	20.6	0.4	51	1	US-08-068-747-1	Sequence 1, Appl1	C 614	20.6	0.4	100	1	US-08-145-705A-3	Sequence 3, Appl1
C 542	20.6	0.4	55	2	PCT-US93-01901-29	Sequence 29, Appl1	615	20.4	0.4	34	4	US-09-085-720-14	Sequence 14, Appl1
C 543	20.6	0.4	56	2	US-08-448-418-63	Sequence 62, Appl1	616	20.4	0.4	41	5	US-09-339-913B-51	Sequence 25, Appl1
C 544	20.6	0.4	59	4	US-09-091-814-62	Sequence 62, Appl1	617	20.4	0.4	62	4	US-09-339-904A-51	Sequence 51, Appl1
C 545	20.6	0.4	61	3	US-09-023-228B-39	Sequence 39, Appl1	618	20.4	0.4	62	4	US-09-769-062B-51	Sequence 51, Appl1
C 546	20.6	0.4	61	3	US-09-163-025B-39	Sequence 39, Appl1	619	20.4	0.4	62	4	US-08-769-062B-51	Sequence 51, Appl1
C 547	20.6	0.4	66	4	US-09-091-814-61	Sequence 61, Appl1	620	20.4	0.4	62	4	US-09-744-002B-51	Sequence 51, Appl1
C 548	20.6	0.4	69	3	US-08-329-799-39	Sequence 39, Appl1	621	20.4	0.4	62	4	US-09-559-565C-51	Sequence 51, Appl1
C 549	20.6	0.4	70	4	US-09-364-380-22	Sequence 22, Appl1	622	20.4	0.4	63	5	PCT-US91-03680-8	Sequence 8, Appl1
C 550	20.6	0.4	72	1	US-07-832-905B-11	Sequence 11, Appl1	623	20.4	0.4	64	2	US-07-814-220-72	Sequence 22, Appl1
C 551	20.6	0.4	72	2	US-08-700-757-11	Sequence 11, Appl1	624	20.4	0.4	64	2	US-07-812-421-22	Sequence 22, Appl1
C 552	20.6	0.4	72	4	US-08-463-691-11	Sequence 11, Appl1	625	20.4	0.4	68	1	US-07-977-284A-234	Sequence 234, Appl1
C 553	20.6	0.4	72	4	US-08-255-235-15	Sequence 15, Appl1	626	20.4	0.4	68	1	US-08-256-426B-234	Sequence 234, Appl1
C 554	20.6	0.4	72	4	US-09-123-728-31	Sequence 31, Appl1	627	20.4	0.4	69	4	US-09-025-769B-153	Sequence 153, Appl1
C 555	20.6	0.4	74	4	US-08-589-109A-4	Sequence 4, Appl1	628	20.4	0.4	70	2	US-08-484-402A-4	Sequence 4, Appl1
C 556	20.6	0.4	75	3	US-08-718-904-93	Sequence 93, Appl1	629	20.4	0.4	70	2	US-08-484-402A-4	Sequence 4, Appl1
C 557	20.6	0.4	75	4	US-08-556-978B-53	Sequence 53, Appl1	630	20.4	0.4	70	2	PCT-US96-09472-4	Sequence 4, Appl1
C 558	20.6	0.4	75	4	US-08-556-978B-54	Sequence 54, Appl1	631	20.4	0.4	71	2	US-08-484-402A-50	Sequence 50, Appl1
C 559	20.6	0.4	77	2	US-08-785-750-10	Sequence 10, Appl1	632	20.4	0.4	71	2	US-08-484-402A-50	Sequence 50, Appl1
C 560	20.6	0.4	77	4	US-09-121-162-4	Sequence 4, Appl1	633	20.4	0.4	71	2	PCT-US96-09472-50	Sequence 50, Appl1
C 561	20.6	0.4	77	4	US-09-205-337-10	Sequence 10, Appl1	634	20.4	0.4	72	2	US-07-812-421-23	Sequence 23, Appl1
C 562	20.6	0.4	81	1	US-08-411-795B-149	Sequence 149, Appl1	635	20.4	0.4	72	2	US-09-173-941-116	Sequence 116, Appl1
C 563	20.6	0.4	81	1	US-08-411-795B-150	Sequence 149, Appl1	636	20.4	0.4	74	3	US-08-430-709-38	Sequence 38, Appl1
C 564	20.6	0.4	81	1	US-08-411-796-149	Sequence 149, Appl1	637	20.4	0.4	77	1	US-07-829-461A-19	Sequence 19, Appl1
C 565	20.6	0.4	81	1	US-08-469-319A-150	Sequence 150, Appl1	638	20.4	0.4	77	2	US-08-918-304A-38	Sequence 38, Appl1
C 566	20.6	0.4	81	1	US-08-469-319A-149	Sequence 149, Appl1	639	20.4	0.4	77	2	US-09-258-797-91	Sequence 91, Appl1
C 567	20.6	0.4	81	2	US-07-989-847-23	Sequence 23, Appl1	640	20.4	0.4	77	4	US-09-407-234-38	Sequence 38, Appl1
C 568	20.6	0.4	81	2	US-08-471-039-149	Sequence 149, Appl1	641	20.4	0.4	77	4	US-09-197-649-20	Sequence 20, Appl1
C 569	20.6	0.4	81	3	US-08-471-039-150	Sequence 150, Appl1	642	20.4	0.4	77	4	US-07-958-232A-4	Sequence 4, Appl1
C 570	20.6	0.4	81	3	US-08-469-411-23	Sequence 23, Appl1	643	20.4	0.4	81	1	US-07-958-232A-4	Sequence 4, Appl1
C 571	20.6	0.4	81	4	US-08-764-114-149	Sequence 149, Appl1	C 644	20.4	0.4	84	4	US-08-461-697-63	Sequence 63, Appl1
C 572	20.6	0.4	81	4	US-08-764-114-150	Sequence 149, Appl1	645	20.4	0.4	85	3	US-08-461-697-63	Sequence 63, Appl1
C 573	20.6	0.4	81	4	US-08-469-419-149	Sequence 149, Appl1	646	20.4	0.4	85	4	US-08-867-921-47	Sequence 47, Appl1
C 574	20.6	0.4	81	4	US-08-469-419-150	Sequence 149, Appl1	C 647	20.4	0.4	88	2	US-08-867-921-47	Sequence 47, Appl1
C 575	20.6	0.4	81	4	US-08-469-419-150	Sequence 149, Appl1	648	20.4	0.4	88	2	US-08-867-921-48	Sequence 48, Appl1
C 576	20.6	0.4	81	5	PCT-US93-11198-149	Sequence 149, Appl1	C 649	20.4	0.4	88	3	US-08-867-921-48	Sequence 48, Appl1
C 577	20.6	0.4	81	5	PCT-US93-11198-150	Sequence 150, Appl1	650	20.4	0.4	88	3	US-09-173-941-116	Sequence 116, Appl1
C 578	20.6	0.4	84	1	US-07-808-451-3	Sequence 3, Appl1	C 651	20.4	0.4	88	4	US-09-393-385B-85	Sequence 85, Appl1
C 579	20.6	0.4	84	1	US-07-808-451-4	Sequence 4, Appl1	C 652	20.4	0.4	88	4	US-09-011-769A-41	Sequence 41, Appl1
C 580	20.6	0.4	84	1	US-07-989-845-19	Sequence 19, Appl1	C 653	20.4	0.4	88	4	US-08-448-194-48	Sequence 48, Appl1
C 581	20.6	0.4	84	1	US-07-989-845-3	Sequence 3, Appl1	C 654	20.4	0.4	89	4	US-08-867-921-48	Sequence 48, Appl1
C 582	20.6	0.4	84	1	US-08-161-044-3	Sequence 3, Appl1	655	20.4	0.4	89	4	US-08-530-569B-14	Sequence 14, Appl1
C 583	20.6	0.4	84	1	US-08-240-121-3	Sequence 3, Appl1	656	20.4	0.4	90	4	US-08-974-549A-695	Sequence 695, Appl1
C 584	20.6	0.4	84	1	US-08-451-241-3	Sequence 3, Appl1	C 657	20.4	0.4	90	4	US-08-974-549A-696	Sequence 696, Appl1
C 585	20.6	0.4	84	1	US-08-443-568B-34	Sequence 34, Appl1	658	20.4	0.4	91	6	5194595-7	Patent No. 5194595
C 586	20.6	0.4	84	1	US-08-443-568B-35	Sequence 35, Appl1	659	20.4	0.4	93	3	US-08-448-194-49	Sequence 49, Appl1
C 587	20.6	0.4	84	5	PCT-US92-10625-3	Sequence 3, Appl1	660	20.4	0.4	93	4	US-08-867-921-49	Sequence 49, Appl1
C 588	20.6	0.4	84	5	PCT-US92-10625-4	Sequence 4, Appl1	661	20.4	0.4	93	5	PCT-US96-01600-16	Sequence 16, Appl1
C 589	20.6	0.4	84	5	PCT-US93-11297-3	Sequence 3, Appl1	662	20.4	0.4	95	1	US-08-479-783A-75	Sequence 75, Appl1
C 590	20.6	0.4	84	5	PCT-US93-11298-19	Sequence 19, Appl1	663	20.4	0.4	95	1	US-08-479-783A-75	Sequence 75, Appl1
C 591	20.6	0.4	84	5	PCT-US94-06997-34	Sequence 34, Appl1	664	20.4	0.4	95	1	US-08-618-653-75	Sequence 75, Appl1
C 592	20.6	0.4	84	5	PCT-US94-06997-35	Sequence 35, Appl1	665	20.4	0.4	95	1	US-08-618-653-75	Sequence 75, Appl1
C 593	20.6	0.4	86	4	US-08-836-261A-10	Sequence 10, Appl1	666	20.4	0.4	95	4	US-08-974-549A-695	Sequence 14, Appl1
C 594	20.6	0.4	87	4	US-08-729-601A-16	Sequence 16, Appl1	667	20.4	0.4	95	5	PCT-US96-08014-164	Sequence 164, Appl1
C 595	20.6	0.4	88	4	US-08-686-968C-126	Sequence 126, Appl1	668	20.4	0.4	97	1	US-08-454-455-1	Sequence 1, Appl1
C 596	20.6	0.4	88	4	US-08-686-968C-133	Sequence 133, Appl1	669	20.4	0.4	99	3	US-08-721-979A-36	Sequence 36, Appl1
C 597	20.6	0.4	88	4	US-08-686-968C-138	Sequence 138, Appl1	670	20.4	0.4	99	3	US-08-836-501-36	Sequence 36, Appl1
C 598	20.6	0.4	88	4	US-08-686-968C-152	Sequence 152, Appl1	671	20.4	0.4	99	4	US-09-654-289-36	Sequence 36, Appl1
C 599	20.6	0.4	88	4	US-08-686-968C-155	Sequence 155, Appl1	C 672	20.4	0.4	100	1	US-08-145-705A-27	Sequence 27, Appl1
C 600	20.6	0.4	89	1	US-08-229-515A-5	Sequence 5, Appl1	C 673	20.4	0.4	100	1	US-08-655-086-3	Sequence 3, Appl1
C 601	20.6	0.4	89	1	US-08-645-865-5	Sequence 5, Appl1	C 674	20.2	0.4	40	4	US-08-991-840A-15	Sequence 15, Appl1
C 602	20.6	0.4	91	1	US-08-317-403A-39	Sequence 39, Appl1	675	20.2	0.4	47	4	US-09-641-638B-876	Sequence 876, Appl1
C 603	20.6	0.4	91	1	US-08-471-985A-39	Sequence 39, Appl1	676	20.2	0.4	47	4	US-09-641-638B-876	Sequence 876, Appl1
C 604	20.6	0.4	91	4	US-09-328-750A-5	Sequence 39, Appl1	677	20.2	0.4	51	4	US-09-401-171C-9	Sequence 9, Appl1
C 605	20.6	0.4	91	5	PCT-US95-12401A-39	Sequence 39, Appl1	C 678	20.2	0.4	57	2	US-08-225-224-9	Sequence 9, Appl1
C 606	20.6	0.4	96	1	US-08-055-917-2	Sequence 2, Appl1	C 679	20.2	0.4	57	2	US-09-018-760-1	Sequence 1, Appl1
C 607	20.6	0.4	96	1	US-08-095-068-2	Sequence 2, Appl1	C 680	20.2	0.4	57	3	US-08-722-258-9	Sequence 9, Appl1
C 608	20.6	0.4	96	1	US-08-140-721A-2	Sequence 2, Appl1	C 681	20.2	0.4	57	3	US-08-993-380-1	Sequence 1, Appl1
C 609	20.6	0.4	96	1	US-08-619-790C-3	Sequence 3, Appl1	C 682	20.2	0.4	57	3	PCT-US95-04468-9	Sequence 9, Appl1
C 610	20.6	0.4	96	2	US-07-785-565A-2	Sequence 2, Appl1	C 683	20.2	0.4	59	3	US-08-918-406-4	Sequence 4, Appl1
C 611	20.6	0.4	96	3	US-08-836-561-60	Sequence 60, Appl1	C 684	20.2	0.4	60	4	US-09-018-138-23	Sequence 23, Appl1

C 685	20.2	0.4	63	2	US-08-658-322-10	Sequence 10, Appl	C 758	20	0.4	56	1	US-08-090-193-22	Sequence 22, Appl
C 686	20.2	0.4	67	1	US-08-318-193-73	Sequence 73, Appl	C 759	20	0.4	56	2	US-08-488-031-22	Sequence 22, Appl
C 687	20.2	0.4	69	1	US-08-215-138-20	Sequence 20, Appl	C 760	20	0.4	56	2	US-08-486-569-22	Sequence 22, Appl
C 688	20.2	0.4	69	1	US-08-407-344-20	Sequence 20, Appl	C 761	20	0.4	56	2	US-08-488-027-22	Sequence 22, Appl
C 689	20.2	0.4	69	3	US-08-480-173A-32	Sequence 32, Appl	C 762	20	0.4	56	2	US-08-090-192-22	Sequence 22, Appl
C 690	20.2	0.4	69	3	US-08-484-408A-32	Sequence 32, Appl	C 763	20	0.4	56	2	US-08-482-663-22	Sequence 22, Appl
C 691	20.2	0.4	70	1	US-07-982-712-23	Sequence 23, Appl	C 764	20	0.4	56	3	US-08-482-658-22	Sequence 22, Appl
C 692	20.2	0.4	72	1	US-08-252-057-26	Sequence 26, Appl	C 765	20	0.4	56	3	US-08-470-349-22	Sequence 22, Appl
C 693	20.2	0.4	74	2	US-08-788-943A-31	Sequence 31, Appl	C 766	20	0.4	56	3	US-08-475-610-22	Sequence 22, Appl
C 694	20.2	0.4	74	2	US-09-341-007B-21	Sequence 21, Appl	C 767	20	0.4	56	3	PCT-US92-00277-22	Sequence 22, Appl
C 695	20.2	0.4	75	2	US-08-788-943A-34	Sequence 34, Appl	C 768	20	0.4	56	5	PCT-US92-00278-22	Sequence 22, Appl
C 696	20.2	0.4	78	3	US-08-388-353-648	Sequence 648, App	C 769	20	0.4	57	1	US-07-916-034-18	Sequence 18, Appl
C 697	20.2	0.4	78	3	US-08-488-551B-648	Sequence 22, Appl	C 770	20	0.4	57	2	US-08-290-731C-8	Sequence 8, Appl
C 698	20.2	0.4	78	3	US-09-288-881-22	Sequence 22, Appl	C 771	20	0.4	58	1	US-07-916-033-63	Sequence 63, Appl
C 699	20.2	0.4	80	1	US-09-543-921-22	Sequence 11, Appl	C 772	20	0.4	58	2	US-08-642-255-75	Sequence 75, Appl
C 700	20.2	0.4	80	1	US-07-796-106-11	Sequence 15, Appl	C 773	20	0.4	58	4	US-08-448-418-64	Sequence 64, Appl
C 701	20.2	0.4	81	3	US-08-458-023B-15	Sequence 73, Appl	C 774	20	0.4	58	4	US-09-502-558-12	Sequence 12, Appl
C 702	20.2	0.4	81	3	US-08-651-136C-73	Sequence 117, App	C 775	20	0.4	60	4	US-09-339-913B-42	Sequence 42, Appl
C 703	20.2	0.4	81	3	US-09-173-941-117	Sequence 73, Appl	C 776	20	0.4	60	4	US-09-339-904A-42	Sequence 42, Appl
C 704	20.2	0.4	81	3	US-09-229-911A-73	Sequence 5, Appl	C 777	20	0.4	60	4	US-08-769-062B-42	Sequence 42, Appl
C 705	20.2	0.4	83	1	US-08-076-090-5	Sequence 5, Appl	C 778	20	0.4	60	4	US-09-344-002B-42	Sequence 42, Appl
C 706	20.2	0.4	83	5	PCT-US94-06661-5	Sequence 40, Appl	C 779	20	0.4	60	4	US-09-559-565C-42	Sequence 42, Appl
C 707	20.2	0.4	85	4	US-09-364-543-40	Sequence 44, Appl	C 780	20	0.4	62	1	US-08-182-175A-99	Sequence 99, Appl
C 708	20.2	0.4	86	1	US-08-471-033-44	Sequence 44, Appl	C 781	20	0.4	62	1	US-08-474-633A-88	Sequence 88, Appl
C 709	20.2	0.4	86	2	US-08-471-044-44	Sequence 44, Appl	C 782	20	0.4	62	4	US-08-823-771-88	Sequence 99, Appl
C 710	20.2	0.4	86	2	US-08-463-483A-44	Sequence 44, Appl	C 783	20	0.4	62	5	PCT-US92-06412-99	Sequence 99, Appl
C 711	20.2	0.4	86	2	US-08-471-046A-44	Sequence 44, Appl	C 784	20	0.4	66	4	US-09-291-874-20	Sequence 20, Appl
C 712	20.2	0.4	86	2	US-08-470-566B-44	Sequence 44, Appl	C 785	20	0.4	66	4	US-09-523-655-36	Sequence 36, Appl
C 713	20.2	0.4	86	2	US-08-469-334-44	Sequence 44, Appl	C 786	20	0.4	68	2	US-08-790-965-87	Sequence 87, Appl
C 714	20.2	0.4	86	3	US-09-300-529-44	Sequence 44, Appl	C 787	20	0.4	68	4	US-09-371-774-87	Sequence 87, Appl
C 715	20.2	0.4	86	4	US-09-335-012-35	Sequence 35, Appl	C 788	20	0.4	69	4	US-08-931-858E-207	Sequence 207, App
C 716	20.2	0.4	86	4	US-09-941-964-95	Sequence 157, App	C 789	20	0.4	70	1	US-08-487-141B-107	Sequence 107, App
C 717	20.2	0.4	87	1	US-08-433-126A-157	Sequence 157, App	C 790	20	0.4	70	2	US-08-927-561-107	Sequence 107, App
C 718	20.2	0.4	87	1	US-08-433-124A-157	Sequence 157, App	C 791	20	0.4	70	2	PCT-US96-09388-107	Sequence 107, App
C 719	20.2	0.4	87	5	US-08-976-413A-157	Sequence 157, App	C 792	20	0.4	71	1	US-08-453-742-3	Sequence 3, Appl
C 720	20.2	0.4	87	5	PCT-US96-06059-157	Sequence 2, Appl	C 793	20	0.4	71	1	US-08-454-464-3	Sequence 3, Appl
C 721	20.2	0.4	88	1	US-07-796-106-2	Sequence 12, Appl	C 794	20	0.4	71	1	US-08-453-222-3	Sequence 3, Appl
C 722	20.2	0.4	88	2	US-07-796-106-12	Sequence 85, Appl	C 795	20	0.4	71	1	US-08-452-802-3	Sequence 3, Appl
C 723	20.2	0.4	88	3	US-08-483-528B-85	Sequence 85, Appl	C 796	20	0.4	71	1	US-08-453-956-3	Sequence 3, Appl
C 724	20.2	0.4	88	3	US-08-673-799C-85	Sequence 85, Appl	C 797	20	0.4	71	1	US-08-086-631-3	Sequence 3, Appl
C 725	20.2	0.4	88	4	US-09-393-385B-85	Sequence 21, Appl	C 798	20	0.4	71	2	US-08-452-930-3	Sequence 3, Appl
C 726	20.2	0.4	90	1	US-08-252-057-21	Sequence 104, App	C 799	20	0.4	71	3	US-08-831-132-17	Sequence 17, Appl
C 727	20.2	0.4	90	1	US-08-184-751-21	Sequence 104, App	C 800	20	0.4	71	4	US-09-416-150-17	Sequence 17, Appl
C 728	20.2	0.4	90	1	US-08-137-117D-104	Sequence 4, Appl	C 801	20	0.4	71	5	PCT-US93-08147-3	Sequence 3, Appl
C 729	20.2	0.4	90	4	US-08-436-717-104	Sequence 73, Appl	C 802	20	0.4	72	2	US-07-814-220-23	Sequence 23, Appl
C 730	20.2	0.4	90	4	US-07-827-691A-4	Sequence 11, Appl	C 803	20	0.4	72	2	US-07-812-421-23	Sequence 23, Appl
C 731	20.2	0.4	90	4	US-08-556-978B-73	Sequence 39, Appl	C 804	20	0.4	74	3	US-08-718-904-97	Sequence 97, Appl
C 732	20.2	0.4	91	5	PCT-US94-08052-11	Sequence 75, Appl	C 805	20	0.4	75	1	US-08-242-098A-19	Sequence 19, Appl
C 733	20.2	0.4	92	2	US-08-392-771-7	Sequence 76, Appl	C 806	20	0.4	75	2	US-07-916-098A-20	Sequence 20, Appl
C 734	20.2	0.4	97	3	US-08-825-852-39	Sequence 41, Appl	C 807	20	0.4	75	2	US-08-723-601A-27	Sequence 27, Appl
C 735	20.2	0.4	97	4	US-09-052-888-39	Sequence 41, Appl	C 808	20	0.4	75	2	US-07-982-712-28	Sequence 28, Appl
C 736	20.2	0.4	99	1	US-08-208-886C-75	Sequence 75, Appl	C 809	20	0.4	80	1	US-07-744-282C-30	Sequence 30, Appl
C 737	20.2	0.4	99	1	US-08-208-886C-75	Sequence 76, Appl	C 810	20	0.4	81	4	US-08-556-978B-70	Sequence 70, Appl
C 738	20.2	0.4	99	1	US-08-378-761A-41	Sequence 76, Appl	C 811	20	0.4	81	4	US-08-556-978B-71	Sequence 71, Appl
C 739	20.2	0.4	99	1	US-08-485-286-41	Sequence 76, Appl	C 812	20	0.4	81	4	PCT-US92-0681A-36	Sequence 36, Appl
C 740	20.2	0.4	99	1	US-08-704-744-75	Sequence 76, Appl	C 813	20	0.4	81	4	US-08-420-443-5	Sequence 5, Appl
C 741	20.2	0.4	99	2	US-08-704-744-75	Sequence 76, Appl	C 814	20	0.4	83	1	US-08-039-778B-10	Sequence 10, Appl
C 742	20.2	0.4	99	2	US-08-483-636-61	Sequence 61, Appl	C 815	20	0.4	86	4	US-09-565-596-17	Sequence 17, Appl
C 743	20.2	0.4	99	2	US-08-483-632-61	Sequence 61, Appl	C 816	20	0.4	86	4	US-09-051-966-2	Sequence 2, Appl
C 744	20.2	0.4	99	3	US-09-070-842A-2	Sequence 2, Appl	C 817	20	0.4	86	4	US-08-247-475-45	Sequence 45, Appl
C 745	20	0.4	28	2	US-08-859-998-500	Sequence 500, App	C 818	20	0.4	90	1	US-08-479-650-45	Sequence 45, Appl
C 746	20	0.4	28	4	US-09-225-928-500	Sequence 10, Appl	C 819	20	0.4	90	1	US-08-191-866D-70	Sequence 70, Appl
C 747	20	0.4	35	4	US-09-297-269-10	Sequence 10, Appl	C 820	20	0.4	90	2	US-08-674-169-45	Sequence 45, Appl
C 748	20	0.4	36	4	US-08-653-648A-55	Sequence 55, Appl	C 821	20	0.4	90	4	US-08-185-949B-70	Sequence 70, Appl
C 749	20	0.4	36	4	US-09-297-269-8	Sequence 8, Appl	C 822	20	0.4	90	4	US-08-974-549A-644	Sequence 644, App
C 750	20	0.4	40	4	US-08-305-764C-42	Sequence 42, Appl	C 823	20	0.4	91	3	US-08-464-700-16	Sequence 16, Appl
C 751	20	0.4	51	3	US-09-462-645C-35	Sequence 35, Appl	C 824	20	0.4	91	3	US-08-825-852-37	Sequence 37, Appl
C 752	20	0.4	51	3	US-08-951-923-48	Sequence 48, Appl	C 825	20	0.4	91	4	US-09-053-868-37	Sequence 37, Appl
C 753	20	0.4	53	1	US-08-429-181-57	Sequence 57, Appl	C 826	20	0.4	92	2	US-08-788-943A-23	Sequence 23, Appl
C 754	20	0.4	53	1	US-08-164-388-57	Sequence 57, Appl	C 827	20	0.4				
C 755	20	0.4	56	1	US-08-211-202-53	Sequence 53, Appl	C 828	20	0.4				
C 756	20	0.4	56	1	US-08-211-202-54	Sequence 54, Appl	C 829	20	0.4				
C 757	20	0.4	56	1	US-08-211-202-58	Sequence 58, Appl	C 830	20	0.4				

831	20	0.4	92	3	US-08-976-413A-419	Sequence 419, App	c 904	19.8	0.4	69	2	US-08-488-161-102	Sequence 102, App
832	20	0.4	93	3	US-08-381-637-28	Sequence 28, App	c 905	19.8	0.4	69	3	US-09-273-685-102	Sequence 102, App
833	20	0.4	93	3	US-08-284-516C-45	Sequence 45, App	c 906	19.8	0.4	69	3	US-08-480-173A-31	Sequence 31, App
834	20	0.4	93	4	US-09-537-911A-45	Sequence 45, App	c 907	19.8	0.4	69	3	US-08-484-408A-31	Sequence 31, App
835	20	0.4	95	2	US-08-525-742-29	Sequence 29, App	c 908	19.8	0.4	69	5	PCT-US95-11934-102	Sequence 102, App
836	20	0.4	96	3	US-08-484-322-20	Sequence 20, App	c 909	19.8	0.4	70	1	US-07-982-712-33	Sequence 33, App
837	20	0.4	97	2	US-08-525-742-27	Sequence 27, App	c 910	19.8	0.4	70	1	US-08-305-699-11	Sequence 11, App
838	20	0.4	98	2	US-08-263-911-21	Sequence 21, App	c 911	19.8	0.4	72	2	US-08-832-466-1	Sequence 1, App
839	20	0.4	98	4	US-08-991-789A-282	Sequence 282, App	c 912	19.8	0.4	72	2	US-08-822-028-56	Sequence 56, App
840	20	0.4	98	4	US-09-062-451-282	Sequence 282, App	c 913	19.8	0.4	72	2	US-08-479-285-56	Sequence 56, App
841	20	0.4	99	2	US-08-611-757-77	Sequence 77, App	c 914	19.8	0.4	72	6	5244792-14	Patent No. 5244792
842	20	0.4	99	3	US-08-721-979A-29	Sequence 29, App	c 915	19.8	0.4	73	1	US-08-453-104-15	Sequence 15, App
843	20	0.4	99	3	US-08-836-501-29	Sequence 29, App	c 916	19.8	0.4	73	1	US-08-175-155-41	Sequence 41, App
844	20	0.4	99	4	US-09-240-078-41	Sequence 41, App	c 917	19.8	0.4	73	1	US-08-477-509B-76	Sequence 76, App
845	20	0.4	99	4	US-09-654-289-29	Sequence 29, App	c 918	19.8	0.4	73	2	US-08-694-824-15	Sequence 15, App
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847	20	0.4	100	4	US-08-974-549A-643	Sequence 643, App	c 920	19.8	0.4	73	4	US-09-444-791A-76	Sequence 76, App
848	19.8	0.4	36	2	US-08-292-620A-1476	Sequence 1476, App	c 921	19.8	0.4	74	1	US-08-260-515-4	Sequence 4, App
849	19.8	0.4	36	3	US-08-585-684B-301	Sequence 301, App	c 922	19.8	0.4	77	1	US-08-384-708A-189	Sequence 189, App
850	19.8	0.4	36	3	US-09-071-845-1476	Sequence 1476, App	c 923	19.8	0.4	77	1	US-08-318-193-62	Sequence 62, App
851	19.8	0.4	36	4	US-09-038-073-301	Sequence 301, App	c 924	19.8	0.4	77	4	US-08-687-421-281	Sequence 281, App
852	19.8	0.4	42	4	US-09-162-484-7	Sequence 7, App	c 925	19.8	0.4	78	1	US-08-053-131-138	Sequence 138, App
853	19.8	0.4	42	4	US-09-641-638-1223	Sequence 1223, App	c 926	19.8	0.4	78	1	US-08-645-641-138	Sequence 138, App
854	19.8	0.4	50	1	US-08-445-640-20	Sequence 20, App	c 927	19.8	0.4	78	1	US-07-853-408B-138	Sequence 138, App
855	19.8	0.4	50	3	US-08-170-558-20	Sequence 20, App	c 928	19.8	0.4	78	1	US-08-096-762-138	Sequence 138, App
856	19.8	0.4	50	3	US-08-447-314-20	Sequence 20, App	c 929	19.8	0.4	78	2	US-08-308-865-138	Sequence 138, App
857	19.8	0.4	50	3	US-08-445-461-20	Sequence 20, App	c 930	19.8	0.4	78	4	US-09-042-353-255	Sequence 255, App
858	19.8	0.4	51	3	US-08-356-965-22	Sequence 22, App	c 931	19.8	0.4	78	4	US-08-758-417A-103	Sequence 103, App
859	19.8	0.4	51	3	US-08-621-700-22	Sequence 22, App	c 932	19.8	0.4	78	4	US-08-979-608A-31	Sequence 31, App
860	19.8	0.4	51	3	US-08-929-940-22	Sequence 22, App	c 933	19.8	0.4	78	5	PCT-US92-10963-138	Sequence 138, App
861	19.8	0.4	51	5	PCT-US95-03964C-51	Sequence 51, App	c 934	19.8	0.4	80	3	US-08-933-983-42	Sequence 42, App
862	19.8	0.4	54	1	US-07-977-696C-51	Sequence 51, App	c 935	19.8	0.4	80	4	US-09-171-945-82	Sequence 82, App
863	19.8	0.4	54	1	US-08-129-930B-51	Sequence 51, App	c 936	19.8	0.4	80	4	US-09-459-427-22	Sequence 22, App
864	19.8	0.4	54	4	US-08-976-288A-51	Sequence 51, App	c 937	19.8	0.4	80	4	US-09-459-427-22	Sequence 22, App
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866	19.8	0.4	55	4	US-09-244-796-12	Sequence 12, App	c 939	19.8	0.4	84	1	US-07-731-157A-33	Sequence 33, App
867	19.8	0.4	57	3	US-08-621-700-16	Sequence 16, App	c 940	19.8	0.4	84	1	US-08-208-886C-34	Sequence 34, App
868	19.8	0.4	57	4	US-08-929-940-16	Sequence 16, App	c 941	19.8	0.4	84	1	US-08-053-131-125	Sequence 125, App
869	19.8	0.4	57	5	PCT-US95-03940-16	Sequence 16, App	c 942	19.8	0.4	84	1	US-08-704-744-32	Sequence 32, App
870	19.8	0.4	60	4	US-09-253-025-10	Sequence 10, App	c 943	19.8	0.4	84	1	US-08-704-744-32	Sequence 32, App
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872	19.8	0.4	61	2	US-08-472-171-54	Sequence 34, App	c 945	19.8	0.4	84	1	US-08-469-557-22	Sequence 22, App
873	19.8	0.4	61	2	US-08-472-171-51	Sequence 50, App	c 946	19.8	0.4	84	1	US-08-469-557-22	Sequence 22, App
874	19.8	0.4	61	2	US-08-483-528B-50	Sequence 50, App	c 947	19.8	0.4	84	1	US-08-469-557-22	Sequence 22, App
875	19.8	0.4	61	2	US-08-894-526-34	Sequence 34, App	c 948	19.8	0.4	84	1	US-07-853-408B-138	Sequence 138, App
876	19.8	0.4	61	2	US-08-894-526-34	Sequence 34, App	c 949	19.8	0.4	84	1	US-08-096-762-125	Sequence 125, App
877	19.8	0.4	61	2	US-09-013-047-34	Sequence 34, App	c 950	19.8	0.4	84	2	US-08-290-793B-34	Sequence 34, App
878	19.8	0.4	61	2	US-08-673-799C-50	Sequence 50, App	c 951	19.8	0.4	84	2	US-08-290-793B-34	Sequence 34, App
879	19.8	0.4	61	3	US-08-673-799C-50	Sequence 50, App	c 952	19.8	0.4	84	2	US-08-308-865-125	Sequence 125, App
880	19.8	0.4	61	3	US-09-374-597-51	Sequence 34, App	c 953	19.8	0.4	84	2	US-08-541-780-33	Sequence 33, App
881	19.8	0.4	61	3	US-09-374-597-51	Sequence 34, App	c 954	19.8	0.4	84	5	PCT-US92-10983-125	Sequence 125, App
882	19.8	0.4	62	1	US-09-393-385B-50	Sequence 50, App	c 955	19.8	0.4	85	1	US-08-627-497-4	Sequence 4, App
883	19.8	0.4	62	1	US-07-593-657-15	Sequence 15, App	c 956	19.8	0.4	85	4	US-09-060-410-11	Sequence 11, App
884	19.8	0.4	63	1	US-07-842-089E-5	Sequence 5, App	c 957	19.8	0.4	85	4	US-09-242-095-6	Sequence 6, App
885	19.8	0.4	63	1	US-08-264-485-5	Sequence 5, App	c 958	19.8	0.4	87	1	US-08-053-131-122	Sequence 122, App
886	19.8	0.4	63	2	US-09-003-081-7	Sequence 7, App	c 959	19.8	0.4	87	1	US-08-645-641-122	Sequence 122, App
887	19.8	0.4	63	3	US-08-648-262-7	Sequence 7, App	c 960	19.8	0.4	87	1	US-07-853-408B-138	Sequence 138, App
888	19.8	0.4	63	3	US-08-648-262-7	Sequence 7, App	c 961	19.8	0.4	87	1	US-08-096-762-122	Sequence 122, App
889	19.8	0.4	64	3	US-08-463-903-53	Sequence 53, App	c 962	19.8	0.4	87	2	US-08-308-865-122	Sequence 122, App
890	19.8	0.4	64	3	US-07-935-695-53	Sequence 33, App	c 963	19.8	0.4	87	4	US-09-208-966-27	Sequence 27, App
891	19.8	0.4	65	1	US-08-484-668B-34	Sequence 34, App	c 964	19.8	0.4	87	4	US-09-042-353-239	Sequence 239, App
892	19.8	0.4	65	1	US-08-484-668B-37	Sequence 37, App	c 965	19.8	0.4	87	4	US-08-758-417A-87	Sequence 87, App
893	19.8	0.4	65	3	US-08-718-904-91	Sequence 91, App	c 966	19.8	0.4	87	5	PCT-US92-10983-122	Sequence 122, App
894	19.8	0.4	65	4	US-08-463-160B-37	Sequence 37, App	c 967	19.8	0.4	88	1	US-07-982-712-33	Sequence 33, App
895	19.8	0.4	65	4	US-08-463-160B-37	Sequence 37, App	c 968	19.8	0.4	88	1	US-08-442-062-30	Sequence 30, App
896	19.8	0.4	65	5	PCT-US91-02568-38	Sequence 38, App	c 969	19.8	0.4	88	1	US-08-748-697A-30	Sequence 30, App
897	19.8	0.4	66	1	US-07-627-539G-4	Sequence 4, App	c 970	19.8	0.4	88	4	US-09-165-616-30	Sequence 30, App
898	19.8	0.4	66	1	US-08-081-539-29	Sequence 29, App	c 971	19.8	0.4	88	4	US-09-171-759-17	Sequence 17, App
899	19.8	0.4	66	1	US-08-466-647-29	Sequence 29, App	c 972	19.8	0.4	88	4	US-09-143-014-7	Sequence 14, App
900	19.8	0.4	66	1	US-08-516-859A-96	Sequence 96, App	c 973	19.8	0.4	88	5	5194596-1	Patent No. 5194596
901	19.8	0.4	66	4	US-09-556-978B-42	Sequence 42, App	c 974	19.8	0.4	88	6	5219739-1	Patent No. 5219739
902	19.8	0.4	66	4	US-09-586-472-96	Sequence 96, App	c 975	19.8	0.4	89	4	US-09-020-956-63	Sequence 63, App
903	19.8	0.4	66	4	US-09-528-706-96	Sequence 96, App	c 976	19.8	0.4	89	4	US-09-030-607-63	Sequence 63, App

[illegible]

; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
 ; TITLE OF INVENTION: Primers Therefor

[illegible]

```

: Sequence 10 Application US/082400498
: Patent No 5686239
:
: GENERAL INFORMATION:
:
: APPLICANT: Reyes, Gregory R.
: APPLICANT: Tam, Albert W.
: APPLICANT: Yarborough, Patricia O.
: TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods

```

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1 Sequence 10 Application US/08240049B
2 Patent No. 5686239
3
4 GENERAL INFORMATION:
5
6 APPLICANT: Reyes, Gregory R.
7 APPLICANT: Tam, Albert W.
8 APPLICANT: Yarbough, Patrice O.
9 TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods
10 NUMBER OF SEQUENCES: 21
11
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Genelabs Technologies, Inc.
14 STREET: 505 Penobscot Drive
15 CITY: Redwood City
16 STATE: CA
17
18 COUNTRY: USA
19
20 ZIP: 94063
21
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Floppy disk
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26 SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28 CURRENT APPLICATION DATA:
29 APPLICATION NUMBER: US/08/240,049B

```

RESULT 4
 US-08-240-049B-10
 : Sequence 10, Application US/08240049B
 Patent No. 5686239
 :
 GENERAL INFORMATION:
 :
 APPLICANT: Reyes, Gregory R.
 :
 APPLICANT: Tam, Albert W.
 :
 APPLICANT: Yarbough, Patrice O.
 :
 TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods
 :
 NUMBER OF SEQUENCES: 21
 :
 CORRESPONDENCE ADDRESS:
 :
 ADDRESSEE: GeneLabs Technologies, Inc.
 :
 STREET: 505 Penobscot Drive
 :
 CITY: Redwood City
 :
 STATE: CA
 :
 COUNTRY: USA
 :
 ZIP: 94063
 :
 COMPUTER READABLE FORM:
 :
 MEDIUM TYPE: Floppy disk
 :
 COMPUTER: IBM PC compatible
 :
 OPERATING SYSTEM: PC-DOS/MS-DOS
 :
 SOFTWARE: Patentin Release #1.0, Version #1.25
 :
 CURRENT APPLICATION DATA:
 :
 APPLICATION NUMBER: US/08/240,049B

RESULT 5
 US-08-542-634-12
 Sequence 12, Application US/08542634
 Patent No. 6214970
 GENERAL INFORMATION:
 APPLICANT: Fuerst, Thomas R.
 APPLICANT: Mcatee, C. Patrick
 APPLICANT: Yarbough, Patrice O.
 APPLICANT: Zhang, Yifan
 TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Ave., Suite 250
 City: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/542,634
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4500-0293.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 99 base pairs
 type: nucleic acid

Query Match	0.5%;	Score 27.4;	DB 4;	Length 99;
INDIVIDUAL ISOLATE:	Hepatitis E Virus (Mexico strain)			
INDIVIDUAL ISOLATE:	406.4-2 region			
US-08-477-292-12				

Best Local Similarity 55.9%; Pred. No. 1.6e+03;
Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 3031 CAGCCGACGATGCGCTGGGCGCAGGCGGCGACGCGGCGGCGAGCGC 3090

Db 7 CAGCCGCGGCGATGCGCTGCGGCGAGATGAGCGCGCGCGCGCTGCGCTGCC 66

Qy 3091 TCCGAGGCGCTGGCGCTGCGTGTGCGCGCGC 3123

Db 67 GTGCGCGACTGCGCAGCGCGGCGCTGCGGCGC 99

RESULT 7

PCT-US95-13703-12

; Sequence 12; Application PC/TUS9513703

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: P.O. Box 60850

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306-0850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/13703

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Fabian, Gary R.

; REGISTRATION NUMBER: 33,875

; REFERENCE/DOCKET NUMBER: 4600-0293.41

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 99 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)

; PCT-US95-13703-12

Query Match 0.5%; Score 27.4; DB 5; Length 99;

Best Local Similarity 55.9%; Pred. No. 1.6e+03;

Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 3031 CAGCCGACGATGCGCTGGGCGCAGGCGGCGACGCGGCGGCGAGCGC 3090

Db 7 CAGCCGCGGCGATGCGCTGCGGCGAGATGAGCGCGCGCGCGCTGCGCTGCC 66

Qy 3091 TCCGAGGCGCTGGCGCTGCGTGTGCGCGCGC 3123

Db 67 GTGCGCGACTGCGCAGCGCGGCGCTGCGGCGC 99

RESULT 8

US-09-242-095-26

; Sequence 26; Application US/09242095

; Patent No. 6277622

; GENERAL INFORMATION:

; APPLICANT: Weiss, Anthony Steven

; TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GRIFFITH HACK

; STREET: LEVEL 8, 168 WALKER STREET

; CITY: NORTH SYDNEY

; STATE: NEW SOUTH WALES

; COUNTRY: AUSTRALIA

; ZIP: 2060

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/242,095

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU P01565

; FILING DATE: 09-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: KURTZ, ANN D

; REGISTRATION NUMBER: N/A

; REFERENCE/DOCKET NUMBER: 24078DM.ADK

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 61 2 9957 5944

; TELEFAX: 61 2 9957 6288

; TELEX: AA 26547

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 96 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "synthetic oligonucleotide"

; HYPOTHETICAL: YES

; ANTI-SENSE: YES

; US-09-242-095-26

Query Match 0.5%; Score 27; DB 4; Length 96;

Best Local Similarity 66.1%; Pred. No. 1.9e+03;

Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 3473 GCCAGAGTTCATGCCCTCGAGCAGCCCGCGAGGCGCAACGACGCTGCC 3531

Db 29 GCCAGAGTTCATGCCCTCGAGGAGTAACCGGAGCGGAGCGGAGAGTGGAGGTGCC 87

RESULT 9

US-09-242-095-13/c

; Sequence 13; Application US/09242095

; Patent No. 6277622

; GENERAL INFORMATION:

; APPLICANT: Weiss, Anthony Steven

; TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GRIFFITH HACK

; STREET: LEVEL 8, 168 WALKER STREET

; CITY: NORTH SYDNEY

; STATE: NEW SOUTH WALES

; COUNTRY: AUSTRALIA

; ZIP: 2060

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 base pairs

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QY 2670 CAGCCGC 2676

Copied from PCI US2003092 on 04-03-2004

Matches	50;	Conservative	0;	Mismatches	43;	Indels	0;	Gaps	0;
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APPLICANT: Lonberg, Nils

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/645,641
FILING DATE: 20-MAY-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
US-08-645-641-129

Query Match 0.5%; Score 24; DB 1; Length 69;
Best Local Similarity 68.8%; Pred. No. 8,56+03;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps:

Cy 4004 CAGGGGACAGGGGTACTGGCTACGACGACGCTCTGGGACAGCATGC 4051
      || |||| | || |||| | |||| | |||| | || |||| |
Db 22 CACTGGGCGCAGGGACCTGTGTCACCGTCTCTCAGGAGATGCATCC 69

RESULT 32
US-07-853-408B-129
Sequence 129, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single

```



```
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10983
FILING DATE: 19921217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US92-10983-129

Query Match          0.5%; Score 24; DB 5; Length 69;
Best Local Similarity 68.8%; Pred. No. 8.5e+03;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 4004 CAGTGGGACAGGGGCTGCTGCTCACCAGCTCTCGGCGACAGCATGC 4051
Db 22 CACTGGGCGCAGGCGACCTGCTGCTCACCAGCTCTCGGCGACAGCATGC 69

RESULT 36
US-09-042-353-249
Sequence 249, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068

FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-0090400S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SBO ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-249

Query Match          0.5%; Score 24; DB 4; Length 72;
Best Local Similarity 68.8%; Pred. No. 8.7e+03;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 4004 CAGTGGGACAGGGGCTGCTGCTCACCAGCTCTCGGCGACAGCATGC 4051
Db 25 CACTGGGCGCAGGCGACCTGCTGCTCACCAGCTCTCGGCGACAGCATGC 72

RESULT 37
US-08-758-417A-97
Sequence 97, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
```

Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-758-417A-97

Query Match 0.5%; Score 24; DB 4; Length 72;
Best Local Similarity 68.8%; Pred. No. 8.7e+03;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4004 CAGTGGGACAGGGGTCGCTCACCACGCTCCTCGGCGACAGCATGC 4051
DB 25 CACTGGGGCGGCGACCCCTGTCACCGTCTCCTCAGGAGTGATGCATCC 72

RESULT 38
US-08-405-702A-5
Sequence 5, Application US/08405702A
Patent No. 5789389
GENERAL INFORMATION:
APPLICANT: Tarasewicz, Dariusz G
APPLICANT: Schott, Brigitte
APPLICANT: Holzmayr, Tatiana A.

APPLICANT: Roninson, Igor B
TITLE OF INVENTION: BCL2 Derived Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,702A
FILING DATE: 17-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5789389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,332
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-405-702A-5

Query Match 0.5%; Score 24; DB 1; Length 84;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2622 GGCCTACCTGACGACCGCCGCTCCTCAGGGATCTCGCCCTTCTCCACCGCCGCTC 2681
DB 3 GGTCCACCTGACCGCTCCGCGGCGGAGAGACTTCTCCGCGCCCTACCGCCGGAATT 62

QY 2682 CAGCGAGCGCTC 2693
DB 63 CCGCGAGATGTC 74

RESULT 39
US-08-405-702A-9
Sequence 9, Application US/08405702A
Patent No. 5789389
GENERAL INFORMATION:
APPLICANT: Tarasewicz, Dariusz G
APPLICANT: Schott, Brigitte
APPLICANT: Holzmayr, Tatiana A.
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: BCL2 Derived Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 40
 US-08-476-176B-22/C
 Sequence 22 Application US/08476176B
 Patent No. 5958708
 GENERAL INFORMATION:
 APPLICANT: Hardman, No. 5958708man
 APPLICANT: Kolbinger, Frank
 APPLICANT: Saldanha, Jose
 TITLE OF INVENTION: Reshaped monoclonal antibodies against an
 TITLE OF INVENTION: Immunoglobulin isotype
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: No. 5958708artis Patent Department
 STREET: 59 Route 10
 CITY: East Hanover
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07936-1080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476,176B
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/127,721
 FILING DATE: 27-SEPTEMBER-1993
 APPLICATION NUMBER: US 07/952,802
 FILING DATE: 25-SEPTEMBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5958708ak, Henry P.
 REGISTRATION NUMBER: 33,200
 REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 277-5110

[illegible]

Search completed: December 11, 2002, 06:15:36
Job time : 140 secs

